

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 17, 2004, 11:33:19 ; Search time 3431 Seconds

(without alignments)
15753.064 Million cell updates/sec

Title: US-09-718-754A-1

Perfect score: 1247

Sequence: 1 atcgactactaagtgcgactt.....agagtcgctagcaactagca 1247

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:
1: gb_ba:*
2: gb_hg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_ph:*
7: gb_pl:*
8: gb_pr:*
9: gb_ro:*
10: gb_st:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_vt:*
15: em_da:*
16: em_fun:*
17: em_hum:*
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21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_st:*
28: em_un:*
29: em_vl:*
30: em_hcg_hum:*
31: em_hcg_inv:*
32: em_hcg_other:*
33: em_hcg_mus:*
34: em_hcg_pln:*
35: em_hcg_rtd:*
36: em_hcg_mam:*
37: em_hcg_vrt:*
38: em_sy:*
39: em_hcgo_hum:*
40: em_hcgo_mus:*
41: em_hcgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	119.2	9.6	7159	8	ZMA437281
2	116	9.3	6588	8	AJ437281 Zea mays
3	108	8.7	6914	8	AY072300
4	106.8	8.6	6128	8	ZMA251453
5	102.4	8.2	9285	8	AJ437282 Zea mays
6	102.2	8.2	133080	2	ZM009989
7	99.4	8.0	147198	8	AC146809
8	99	7.9	4695	6	AF466203
9	99	7.9	4695	6	AF6563
10	98.6	7.9	183502	2	ZMPHYT1
11	97.8	7.8	6588	8	AC145227
12	97	7.8	226001	8	AY072300
13	92	7.4	135556	2	AF391808
14	88.4	7.1	113950	2	AC147603
15	88	6.3	318	6	AC114395
16	78.2	6.3	113950	2	AR252208
17	77.6	6.2	6506	8	AF434193
18	70.8	5.7	226001	8	AF391808
19	70.4	5.6	135556	2	AC147603
20	69.6	5.6	70679	2	AC147518
21	67.2	5.4	15783	8	AF347696
22	67.2	5.4	15783	8	AF434192
23	67.2	5.4	113950	2	AC114395
24	64.4	5.2	258658	3	AB014832
25	62.6	5.0	13868	6	AX027357
26	62.4	5.0	348600	1	AB063521
27	62.2	5.0	266371	2	AC020619
28	61.8	5.0	177650	9	AC104027
29	60	4.8	20063	8	CGP51533
30	59.8	4.8	110000	2	AC116984_3
31	58.8	4.7	181415	2	AC145262
32	58.4	4.7	349751	3	PFMAL4P3
33	58.2	4.7	1219	3	AF513853
34	58	4.7	5689	6	AX251180
35	58	4.7	5689	6	AX277927
36	58	4.7	5689	6	AX323612
37	57.8	4.6	854	9	HSU85253
38	57.8	4.6	1241	8	MITGVARI
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40	57.2	4.6	105574	2	AC013308
41	57.2	4.6	170237	9	AL137070
42	57.2	4.6	333321	3	AC116986
43	56.8	4.6	1986	8	AF305892
44	56.4	4.5	67970	3	PFMALIP3
45	56.4	4.5	169546	2	AC004157

ALIGNMENTS

RESULT 1
LOCUS ZMA437281 7159 bp DNA linear PLN 27-NOV-2003
DEFINITION Zea mays ZmEBE-1 gene for ZmEBE-1 protein, exons 1-5.
ACCESSION AJ437281
VERSION AJ437281.1 GI:28569665
KEYWORDS ZmEBE-1 gene; ZmEBE-1 protein.
SOURCE Zea mays
ORGANISM Zea mays
Bukariyola, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 Magnard, J. L., Lehoucq, G., Massonneau, A., Heckel, T.,
Gutierrez-Marcos, J., Gomez, E., Perez, P., Dumas, C. and Rogowsky, P. M.

JOURNAL	REFERENCE	AUTHORS	TITLE
JOURNAL	2 (bases 1 to 7159)	Rogowsky, P.M.	ZmDd1a and ZmDd1b: two novel genes specifically expressed in the embryo sac and the basal endosperm transfer layer of maize
JOURNAL	Submitted (26-FEB-2002)	Rogowsky P.M., RDP, ENS-Lyon, 46 Allée d'Italie, F-69364 Lyon Cedex 07, FRANCE	Direct Submission
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exon	3582..3778	/gene="ZmBBE-1"	
CDS	join(3596..3778,4489..4668,4742..4795,4875..5012,6181..6540)	/gene="ZmBBE-1"	
exon	3779..4488	/gene="ZmBBE-1"	
intron	4489..4668	/gene="ZmBBE-1"	
exon	4669..4741	/gene="ZmBBE-1"	
intron	4742..4795	/gene="ZmBBE-1"	
exon	4796..4874	/gene="ZmBBE-1"	
intron	4875..5012	/gene="ZmBBE-1"	
exon	5013..6180	/gene="ZmBBE-1"	
intron	6181..6730	/gene="ZmBBE-1"	
exon	6731..7159	/gene="ZmBBE-1"	
ORIGIN	Query Match	9.6%; Score 119.2; DB 8; Length 7159;	
Db	Best Local Similarity	70.9%; Pred. No. 5.7e-17;	
Qy	Matches 190; Conservative 0; Mismatches 68; Indels 10; Gaps 2;		
Db	2362	CTAATCCAGATATTAGTAGAGATGTTAGTAGAT-TAAGTGATGTTGAATGACT	321
Qy	322	AGAGCTAATATTGAGTAAATTAATTTGAGAGACATCAACACCTA-----T	372
Db	2422	AGAGCTAATATTGAGTAAATTAATTTGAGAGACATCAACACCTTACGTTAATGTT	2481

Query Match	Score	DB	Length
Best Local Similarity	74.2%	Pred. No. 3.1e-15	

Query	DB	Score	DB	Length
373 CAATTATTAGTATTATTTAGTAATAGTATATAGTATTAGTATTATTAAGCTACCT	432			
2482 CAACTATTAGCTATTTTATAGTAATATAGTATATAGTATAGCTATTTGTTAGTTAGTT	2541			
433 TTTTCTCTAGCAATTTTTAGCCAACTAACAAATTAAGTTTAAAGTATCAAAATGCCCT	492			
2542 AATTCCTACGTACCAATTTTATAGCCAACTAATTAATAGCTGAGTGCATTCACACCCCTAA	2601			
493 AAGCGTTAAGTAGTATGCTCTTTCTAGAA	520			
2602 AGAAGATGGACACGATCTAGCGCGTAA	2629			

RESULT 2	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE	AUTHORS	TITLE	JOURNAL
AY072300	6588 bp	DNA	linear	PLN 15-JUL-2002											
AY072300		Zea mays subsp. mays cytochrome P450 monooxygenase CYP72A5 gene,													
AY072300.1	GI:21805644														
		Zea mays subsp. mays (maize)													
		Zea mays subsp. mays													
		Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.													
		1 (bases 1 to 6588)													
		Mang J., and Schuler, M.A.													
		Molecular characterization of the maize CYP71C3 and CYP72A subfamily genes													
		Unpublished													
		2 (bases 1 to 6588)													
		Mang J., Reeds, R., and Schuler, M.A.													
		Xenobiotics regulate maize cytochrome P450 monooxygenases at a post-transcriptional level													
		Unpublished													
		3 (bases 1 to 6588)													
		Mang, J., and Schuler, M.A.													
		Submitted (02-JAN-2002) Department of Cell and Structural Biology, University of Illinois at CU, 601 S. Goodwin Ave., Urbana, IL 61801, USA													
		Location/Qualifiers													
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		/organism="Zea mays subsp. mays"													
		/mol_type="genomic DNA"													
		/cultivar="Indred B73"													
		/sub_species="mays"													
		/db_xref="taxon:4578"													
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Db 4100 T-TAAACATCCAAACATCATAGCTAATAGTTAGTATTAACTATTATTAGTAATAGT 4042

QY 402 TTAATGTTAGTATGTTATTTAAGTACTTTTATAGCAATTTTATAGCCAACTA 461

Db 4041 TTAATGTTAGTATGTTATTTAGTACTAATTAAGTAACTAATTAATTTAGCCAACTA 3983

QY 462 ACAATTAGTTTATGTTATTTCAATACC 489

Db 3982 ACTATTAGTTCTTAATGATCAATCAACACC 3955

RESULT 4
ZMA437282 6128 bp DNA linear PLN 27-NOV-2003
LOCUS Zma mays ZmEBE-2 gene for ZmEBE-2 protein, exons 1-4.
ACCESSION AJ437282.1 GI:28569667
VERSION ZmEBE-2 gene; ZmEBE-2 protein.
KEYWORDS Zea mays
SOURCE Zea mays
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
AUTHORS Magnard,J.L., Lehouque,G., Massonneau,A., Heckel,T., Gutierrez-Marcos,J., Gomez,E., Perez,P., Dumas,C. and Rogowsky,P.M.
TITLE ZmEBE-2 gene and the basal endosperm transfer layer of maize embryo sac and the basal endosperm transfer layer of maize
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 6128)
AUTHORS Rogowsky,P.M.
TITLE Direct Submission
JOURNAL Submitted (26-FEB-2002) Rogowsky P.M., RDP, ENS-Lyon, 46 Allée d'Italie, F-69364 Lyon Cedex 07, FRANCE
FEATURES
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/db_xref="taxon:4577"
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/codon_start=1
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/db_xref="GI:28569668"
/db_xref="SPTREMBL:Q84V09"
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/gene="ZmEBE-2"
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intron 4240..5098

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ORIGIN
Query Match 8.6%; Score 106.8; DB 8; Length 6128;
Best Local Similarity 76.4%; Pred. No. 4.3e-14;
Matches 162; Conservative 0; Mismatches 37; Indels 13; Gaps 2;

QY 293 TATGATTAGGTGATGTTTGATGCACCTAGACGTAATAGTATGCTAAATATGTTG 352

Db 5913 TAAGATTATGCGGTGTTGAATGATATAGAGCTAAATATAGCGCTAAATAATAGTTG 5854

QY 353 GAGACATTCAAACACCCCA-----TCATTATGTTATTTTGTGTAATATGTTA 403

Db 5853 AAGACATCCAAACACTGCTAGCTAAATAGTACGCTAATGCTATTTTGTGTAATATGTTA 5794

QY 404 ATAGT----TAGTATGTTATTTATATAGCTAGCTTTTATCTAGCAATTTTATAGCCAA 459

Db 5793 ATAGTATGCTAGCTAGATATTTGTTAGTATGCTATTTCTAGTAAATTTTATAGCAAT 5734

QY 460 TAACAATTAGTTTATGCTATTCATCAATACCC 491

Db 5733 TAAATATTAGCTCTAGTACATTTAAACACCTC 5702

RESULT 5
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LOCUS Zma mays D3L H(+) -transporting AtPase (Mha1) gene, complete cds.
DEFINITION Zea mays D3L H(+) -transporting AtPase (Mha1) gene, complete cds.
ACCESSION U09989
VERSION U09989.1 GI:507770
KEYWORDS
SOURCE Zea mays
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
AUTHORS Jin,Y.K. and Bennetzen,J.L.
TITLE Integration and nonrandom mutation of a plasma membrane proton ATPase gene fragment within the Bgl retroelement of maize
JOURNAL Plant Cell 6 (8), 1177-1186 (1994)
MEDLINE 95003707
PUBMED 7919987
REFERENCE 2 (bases 1 to 9285)
AUTHORS Jin,Y.
TITLE Direct Submission
JOURNAL Submitted (24-MAY-1994) Young-Kwan Jin, Biological Sciences, Purdue University, 339 Hansen Life Science Research Building, West Lafayette, IN 47907, USA
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3722..3844,3927..4031,4113..4257,4379..4543,4637..4875,
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Beet Local Similarity 75.7%; Pred. No. 4.7e-13;
Matches 156; Conservative 0; Mismatches 41; Indels 9; Gaps 2;

QY 294 ATAGATTAGTATGATGTTGAATGCACTAGACCTAATAGTATAGTAAATAGTTGG 353
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DB 6622 AAAAAAAGGAGAGGTTTGAATGCACTAGAAATATATAGTACGACCTAAATTTGTTA 6681
    |||||

QY 354 AGACATTCAAACACCTATCAATATATAGTTATTTTACTA-----AATTAGTTAAT 405
    |||||
DB 6682 AGACATTCAAACACCTATCAATATAGTTATATTAATTAATTAATTAATTAAT 6741
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QY 406 AGTTGTAGTATATATATAGCTAGCTTTTCTTACTAGCAATTTTACCAACTAACAA 465
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DB 6742 AGTTGTAGTATATATATAGCTAGCTAATTTTCACTACCAATTTTACCAACTAACAA 6800
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QY 466 TTAGTTTGTAGTATTCATCAATATACCC 491
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DB 6801 TTAGATCTATATCATTCATTCAAACACAC 6826
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RESULT 6
AC146809      133080 bp      DNA      linear      HTG 26-NOV-2003
LOCUS
DEFINITION   Zea mays clone ZMMBB0355F08, *** SEQUENCING IN PROGRESS ***, 5
unordered pieces.
ACCESSION   AC146809
VERSION     AC146809.2 GI:38348713
KEYWORDS    HTG; HTGS_PHASE1; HTGS_FULFLOP; HTGS_ACTIVEFIN.
SOURCE      Zea mays
ORGANISM    Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 133080)
Birren,B., Nusbbaum,C., Lander,E., Butler,E., Wang,R., Bharti,A.K.
and Messing,J.
Zea mays, clone ZMMBB0355F08
Unpublished
2 (bases 1 to 133080)
Birren,B., Nusbbaum,C., Lander,E., Abouelleil,A., Allen,N.,
Anderson,M., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
Boguslavskiy,L., Boukhalter,B., Camarata,J., Chang,J., Choepel,Y.,
Collimore,A., Cook,A., Cooke,P., Corum,B., Dearellano,K.,
Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S.,
Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
Lindblad-Toh,K., Liu,G., Lui,X., Mabbitt,R., Maclean,C.,
Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
McDonald,P., Meneus,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J.,
Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
O'Neill,D., Oliver,J., Peterson,K., Phunhahng,P., Pierre,N.,
Rachupka,A., Ramsamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Schauer,S., Schnupack,R., Seaman,S., Severy,P., Smith,C.,
Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
Talamas,J., Testaye,S., Theodore,J., Topham,K., Travers,M.,
Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (08-OCT-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 133080)

```

AUTHORS

Birren,B., Nusbbaum,C., Lander,E., Abouelleil,A., Allen,N.,
Anderson,M., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
Boguslavskiy,L., Boukhalter,B., Camarata,J., Chang,J., Choepel,Y.,
Collimore,A., Cook,A., Cooke,P., Corum,B., Dearellano,K.,
Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S.,
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Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A., Zody,M.,
Butler,E., Wang,R., Bharti,A.K. and Messing,J.

TITLE

JOURNAL

Submitted (26-NOV-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Nov 16, 2003 this sequence version replaced gi:37574225.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

COMMENT

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIRB
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu

Bharti, AK and Messing, J. The Plant Genome Initiative at
Rutgers, Waksman Institute, Rutgers, The State University of New
Jersey, 190 Frelinghuysen Road, Piscataway, NJ 08854, USA
(<http://pgr.rutgers.edu>)

Butler, E and Wang, R: Arizona Genomics Institute, Biological
Sciences West, 448A, P.O. Box 210088, University of Arizona,
Tucson, AZ 85721, USA (<http://www.genome.arizona.edu>)

Project Information

Center project name: 355_F_8

Center clone name: L29774

* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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119446 119545: gap of 100 bp
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128392 128491: gap of 100 bp
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ORGANISM	protein	putative pol protein	putative gag		
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AUTHORS	Llaca, V., Linton, E.W., Young, S., Kovchok, S. and Messing, J.				
TITLE	Direct Submission				
JOURNAL	Submitted (07-JAN-2002) Rutgers, The State University of New Jersey				
REFERENCE	190 Frlinghuysen Road, Piscataway, NJ 08854, USA				
AUTHORS	2 (bases 1 to 147198)				
TITLE	Ramakrishna, W., Sanmiguell, P., Emberton, J. and Bennerzen, J.				
JOURNAL	Direct Submission				
REFERENCE	Submitted (07-JAN-2002) Department of Biological Sciences, Purdue University, West Lafayette, IN 47907, USA				
AUTHORS	Location/Qualifiers				
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Db 27276 AATTAGTATTTTATGTAATTAGCTATTGACAAATTGACAAATTAGCTAAT 27217

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ACCESSION A69563.1 GI:4774196
VERSION A69563.1
KEYWORDS
SOURCE unclassified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 4695)
AUTHORS Mangest,S., Perez,P. and Lescaure,A.
TITLE PLANT PHYTASES AND BIOTECHNOLOGICAL APPLICATIONS
JOURNAL Patent: WO 9805785-A 2 12-FEB-1998;
AGRONOMIQUE INST NAT RECH (FR)
COMMENT Other publication FR 2751987 19980206.
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ORIGIN
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VERSION	AJ223470.1	GI:3955064	
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ORGANISM	Zea mays		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.		
AUTHORS	1		
TITLE	Maugeneat, S., Martinez, I., Godin, B., Perez, P. and Leasure, A.M.		
JOURNAL	Structure of two maize phyase genes and their spatio-temporal		
MELINES	expression during seedling development		
PUBMED	Plant Mol. Biol. 39 (3), 503-514 (1999)		
REFERENCE	99190599		
AUTHORS	2 (bases 1 to 4695)		
TITLE	Leasure, A.		
JOURNAL	Direct Submission		
FEATURES	Submitted (15-JUN-1998) Leasure A., Laboratoire de biologie des		
source	semences, INRA, Route de saint Cyr, Versailles 78026 Cedex, FRANCE		
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DB	1247	GT---TAGCTAAATTTGCTAGACACTTCAACACCTATAGCTAATATATAGTTAGC	1191	
OY	377	TATTAGTATTTTACTAAATTTAGTTAATAGTTAGTATTTATTTATAGTACTTTT	436	
DB	1190	TATTACATTTTTTAGTAATTTAGCTACTGCTGTTAGTACATATTTGTTAGTTACTAAT	1131	
OY	437	TTACTAGCAATTTTTTACCACTAACAATTTAGTTAGTGTATTTCAATACCC	491	
DB	1130	CTACTAGTATTTTGTAGCTGACTACTAATTTAGCTCTAGTGCATTTCAACACCC	1076	
RESULT 10				
AC145227		183502 bp	DNA	linear HTG 09-OCT-2003
LOCUS				
DEFINITION				Zeae mays clone ZMMB0045A01, *** SEQUENCING IN PROGRESS ***
ACCESSION				AC145227.3
VERSION				GI:37059943
KEYWORDS				HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.
SOURCE				Zeae mays
ORGANISM				Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE				1 (bases 1 to 183502)
AUTHORS				Bitren,B., Nusbbaum,C., Lander,E., Butler,E., Wing,R., Bharti,A.K. and Messing,J.
TITLE				Zeae mays clone ZMMB0045A01
JOURNAL				Unpublished
REFERENCE				2 (bases 1 to 183502)
AUTHORS				Bitren,B., Nusbbaum,C., Lander,E., Abouelleil,A., Allen,N., Anderson,M., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhalter,B., Camarata,J., Chang,J., Choepel,Y., Collymore,A., Cook,A., Cooke,P., Corum,B., Dearellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galejan,J., Gardyos,B., Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagoos,B., Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kanat,A., Karatas,A., Kells,C., Lander,T., Levine,R., Lindblad-Toh,K., Liu,X., Lui,A., Mabbitt,R., Maclean,C., McDonald,P., Major,J., Manning,T., Matthews,C., McCarthy,M., Melidrom,D., Meneses,L., Mahova,T., Menga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schupbach,R., Seeman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
TITLE				Direct Submission
JOURNAL				Submitted (17-JUN-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE				3 (bases 1 to 183502)
AUTHORS				Bitren,B., Nusbbaum,C., Lander,E., Abouelleil,A., Allen,N., Anderson,M., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhalter,B., Camarata,J., Chang,J., Choepel,Y., Collymore,A., Cook,A., Cooke,P., Corum,B., Dearellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galejan,J., Gardyos,B., Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagoos,B., Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kanat,A., Karatas,A., Kells,C., Lander,T., Levine,R., Lindblad-Toh,K., Liu,X., Lui,A., Mabbitt,R., Maclean,C., McDonald,P., Major,J., Manning,T., Matthews,C., McCarthy,M., Melidrom,D., Meneses,L., Mahova,T., Menga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schupbach,R., Seeman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

QY	304	GTGATGTTGGAATGACATAGAGCTAATAGTATAGTAAATAGTTAGGACATTCAA	363
Db	6243	GGGGTGTTCATGACACAGAGTCAATATGTATGTGCTAAATATATGTTGAAATATATCTAA	6184
QY	364	ACACCCTA-----TCAATTTATAGTTATTTTATAGTAATATAGTTAATAGTTAGTTA	414
Db	6183	ACATTTGATCTCAATAGTTCACACTATATGTTACTTTTATAGTAATATAGCAATAGTTGGCTA	6124
QY	415	GTATATTTAATAGCTAGCTTTTATTTACTAGCAATTTTATAGCCAACTAACTAATAGTTTAA	474
Db	6123	GCTATTTGTTGTTGCTAACAATATTTATTTATTTATTTTATTTTATTTAGCCAACTAAC--TAGCTCTA	6067
QY	475	GTGATTTCAATATACCCCTTAG	495
Db	6066	GTACATTCACAAACCCCTTTAG	6046
RESULT 12			
LOCUS	AF391808/c		
DEFINITION	Zea mays	226001 bp	DNA linear
ACCESSION	AF391808	AF296123	AF320086
VERSION	AF391808.2	GI:17082476	
KEYWORDS			
SOURCE			
ORGANISM			
	Zea mays		
	Zea mays		
	Eumariotaxa, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.		
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FEATURES	source
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COMMENT	/db_xref="taxon:4577"
FEATURES	/chromosome="9"
source	/map="9S"
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CDS	join(21. .178,283. .478,1451. .1927,3754. .3942)
gene	/product="hypothetical protein 4"
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CDS	/protein_id="AAK73104.1"
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mRNA	/translation="MSDQALFSMKRAAPHDKCPRAVGRRIQTESRRHHYHPRNELLPPTPQSDPRTTPCARASRSPRARAAARATSPPCSAAREPPSPSLSRQPPEPGGPPRRASPPRRSSSSSRPRLAELELRVRRVSGAGGYTMMRHGCTGPRYAKVLVIGNHDDVRRQIAKEIAILRTAEHPAVVCHGMTEEGEGLDILBYMDGSLDNRITAEPLADVGQVLSGLAYLHRRLVHRDIKFSNLIIDSARVKLIADFGVGRILNTRDIPCNSSVGTIAVMSPERINTDLNDSYDYGADISFGLSILEFYLGFPFCEBNIQRQDGMALMCAICYNDDPEPDPPTASRFGRFIACCLQKPAKRULTAOLLQHPVACGHPRIAAPPS"
gene	complement(12719. .14404)
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CDS	complement(join(12719. .13170,13252. .14404))
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           SSSDNEGLATTATFNKSAIPNEHHTCMAREKKSVPRTSTVASSSDESDIED
           YSCLRKGLDRTYDKINELIDALNDKRLLEKQEDLLYEHKPTVBAQSLALETKRN
           EMUSCLSTCHDSISLSKINDLNKLEIASKINSREHVTICRCKDFNDACSEH
           HVCISLNDENVASLNAQLKTSKNDPKLKFADAYTVGHHPTKGLGFKRAKNLIS
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           31018..31022
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Query Match 7.8%; Score 97; DB 8; Length 226001;
 Best Local Similarity 77.6%; Pred. No. 1.2e-11;
 Matches 159; Conservative 0; Mismatches 35; Indels 11; Gaps 3;

LAPSEADPTPEPGVVSFTPEHBERGFMSPASRFMRALPHYGVGFHNFNNSIAQAA

```

QY 226 AGATTAAAGGTATGTTTGAATGCACTAGAGCTAATAGTAGAGTAAATAGTTGGG 355
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Db 4740 AGTATTAGACACVGTGTTTAATGACACTAGAGCTAGAGTGTGCTGAATAATTGAAATTA- 4682
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 356 ACATTCAAAACACCCCTA-----TCATTATTAGTATTATTTTGTAAATAGTTAATA 406
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4681 ACATCAAAACAGCTCACTAATAGTTCACACTATTATTTTGAATAGTAAATAGTAA 4622
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QY 407 GTTAGTATTAGTATTATTAAGCTAGCTTTTCTTACTAGCAATTTTATGACCACTAAT 466
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4621 GTTAGCTAGATTAATTTGTTTACCTAGCTAATTTTCACTACCA--TTTATGACCACTAATAT 4563
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 467 TAGTTTAGTGTATCAATATCCCC 491
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RESULT 13
 AC147603/c 135556 bp DNA linear HTG 19-DEC-2003
 LOCUS Zea mays clone ZMMBc00-307D13, *** SEQUENCING IN PROGRESS ***, 6
 DEFINITION unordered pieces.
 AC147603
 VERSION AC147603.1 GI:40217705
 KEYWORDS HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
 clade; Panicoidae; Andropogoneae; Zea.
 1 (bases 1 to 135556)
 Birren,B., Nussbaum,C. and Lander,E.
 Zea mays, clone ZMMBc00-307D13
 Unpublished
 2 (bases 1 to 135556)

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS

Birren,B., Nussbaum,C., Lander,E., Abouelleil,A., Allen,N.,
 Anderson,M., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
 Boguslavskiy,L., Bounghalter,B., Camarata,S.J., Chang,J., Choepel,Y.,
 Collymore,A., Cook,A., Cooke,P., Corum,B., DeBellano,J.,
 Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
 Ferreira,P., Fitzgerald,M., Gage,D., Hagopian,D., Haggan,S.,
 Graham,L., Grand-Pierre,N., Hafez,N., Johnson,R., Jones,C.,
 Hall,J., Horton,J., Hulme,M., Iliev,I., Johnson,R., Jones,C.,
 Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
 Lindblad-Toh,K., Liu,X., Lui,A., Mabbitt,R., McClean,C.,
 MacDonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
 Meldrum,J., Menees,L., Mihova,T., Mlangwa,V., Murphy,T., Naylor,J.,
 Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
 O'Neill,D., Oliver,J., Peterson,K., Phunhahang,P., Pierre,N.,
 Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
 Roman,J., Schauer,S., Schupack,R., Seaman,S., Severy,P., Smith,C.,
 Spencer,B., Strange-Thomann,N., Stojanovic,N., Stubbs,M.,
 Talama,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
 Vasilev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
 Wymann,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
 Direct Submission
 Submitted (19-DEC-2003) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 ALL repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WMR
 Web site: http://www-seg.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information

TITLE
 JOURNAL
 COMMENT

Center Project name: L30037
Center Clone name: 307_D13

* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 54479: contig of 54479 bp in length
* 54480 54579: gap of 100 bp
* 54580 72710: contig of 18131 bp in length
* 72711 72810: gap of 100 bp
* 72811 75699: contig of 2889 bp in length
* 75700 75799: gap of 100 bp
* 75800 87618: contig of 11819 bp in length
* 87619 87719: gap of 100 bp
* 87719 128387: contig of 40669 bp in length
* 128388 128487: gap of 100 bp
* 128488 135556: contig of 7069 bp in length.
Location/Qualifiers

1.135556
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/mol_type="genomic DNA"
/db_xref="taxon:4577"
/clone="ZMBEB00-307D13"
/clone_1ib="CHORI EcorI BAC Library"

ORIGIN

Query Match 7.4%; Score 92; DB 2; Length 135556;

Best Local Similarity 55.5%; Pred. No. 1.7e-10; Indels 10; Gaps 5;
Matches 281; Conservative 0; Mismatches 215;

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* Oy 305 TATGTTAATGACATAGCTAATAGTATAGTAAATAGTTGAGACATTCAAA 364
Db 49407 TATGTTAATGACATAGCTAATAGTATAGTAAATAGTTGAGACATTCAAA 49348
Oy 365 CACCCTATCAATATTAGTATTAGTAAATAGTATAGTATAGTATATTATA 424
Db 49347 TATGTTAATGACATAGCTAATAGTATAGTAAATAGTATAGTATATTATA 49288
Oy 425 AGCTAGCTTTTATAGCAATTTTATAGCCACTAACATAGTTTATAGTATTTCA 484
Db 49287 TATGTTAATGACATAGCTAATAGTATAGTAAATAGTATAGTATATTATA 49228
Oy 485 ATACCCCTAAGCGGTAAAGTATCTCTTCTAGAAATCTTAACGTATGAGACACA 544
Db 49227 AGCGGAAAACTTCACTGCGCGCTTAATTAAGAA----AACCGCACTGAAAAAGTGA 49172
Oy 545 TTTTCATAGGTGATG-TTTAAGTACCGTCAGTATATATATTTTCACTGCGGTT 603
Db 49171 TTTTCATAGGTGATG-TTTAAGTACCGTCAGTATATATATTTTCACTGCGGTT 49112
Oy 604 TCTTAAGCAACCGCGCAGTCTATATATTTTCACTAGCGGCTCTTAAGAAACCGC 663
Db 49111 TCTTAAGCAACCGCGCAGTCTATATATTTTCACTAGCGGCTCTTAAGAAACCGC 49053
Oy 664 CCGTCTAAGATATTATTAAGTCTAGCGGTGTAACAAGTCTGTAAGAAAAAGCGGATT 723
Db 49052 CAGTGAATAATGACATTTTCACTGCGGCTTCAAAATTAACCGCGGATG-GAATGCTGATT 48994
Oy 724 CCTACTAGCCCTAGCTGCACTGCGACATATAAAAGCTCAGTGAATAAGCTTAGGA 783
Db 48993 TCCACTGACCCCTAGC---ACTGCGGATCTGAAAAACCGCAGTGTAAATAGGTTAGAA 48937
Oy 784 TGTCTACTATAGAGCTTCTATGACT 809
Db 48936 CCGCAGCTATAGAGCTTCTGTAAT 48911

```

RESULT 14

AC114395/c

LOCUS AC114395 113950 bp DNA linear HTG 27-MAR-2002

DEFINITION Zea mays chromosome unknown clone ZM06E22, *** SEQUENCING IN

AC114395

PROGRESS ***, 9 ordered pieces.

AC114395

AC114395.2

GI:19745056

HTG: HTGS_PHASE2.

Ze mays

ORGANISM

Ze mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD

clade; Panicoidae; Andropogoneae; Zea.

1 (bases 1 to 113950)

Jiang, J., Nagaki, K., Yuan, Q., Vanaken, S., Uterbach, T.,

Gansberger, K. and Buell, R.

Ze mays BAC clone ZM06E22 BAC genomic sequence

Unpublished

2 (bases 1 to 113950)

Buell, R.

Direct Submission

Submitted (08-MAR-2002) The Institute for Genomic Research, 9712

Medical Center Dr, Rockville, MD 20850, USA

3 (bases 1 to 113950)

Jiang, J., Nagaki, K., Yuan, Q., Vanaken, S., Uterbach, T.,

Gansberger, K. and Buell, R.

Direct Submission

Submitted (27-MAR-2002) University of Wisconsin, Department of

Horticulture, Madison, WI 53706, USA

On Mar 27, 2002 this sequence version replaced gi:19263254.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 9 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submitter.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

1 12871: contig of 12871 bp in length

1 12872: gap of unknown length

1 12972: contig of 13557 bp in length

1 26529: gap of unknown length

1 26629: gap of unknown length

1 27838: gap of 1209 bp in length

1 27938: gap of unknown length

1 27938: gap of 5953 bp in length

1 33891: gap of unknown length

1 33991: gap of 1421 bp in length

1 35412: gap of unknown length

1 35512: gap of 568 bp in length

1 36080: gap of unknown length

1 36180: gap of 4118 bp in length

1 77298: gap of unknown length

1 77397: gap of 8755 bp in length

1 86122: gap of unknown length

1 86223: gap of 27728 bp in length.

Location/Qualifiers

1.113950

/organism="Zea mays"

/mol_type="genomic DNA"

/db_xref="taxon:4577"

/chromosome="unknown"

/clone="ZM06E22"

/note="The BAC contains DNA sequences associated with

maize centromeres."

ORIGIN

Query Match 7.1%; Score 88.4; DB 2; Length 113950;

Best Local Similarity 66.1%; Pred. No. 1.1e-09; Indels 6; Gaps 4;
Matches 189; Conservative 0; Mismatches 91;

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Oy 525 AACCGTATGAGACAAATTTTATAGTGTAGTCTG-TTTAAGTACCGTCAGTATGA 583
Db 21613 AACCGCAGTGAAGATGATTTTCAAGTGGCGGTTTGTATTATAAACCGCGAGTGA 21554

```

QY 584 TATATTTTCACATGCGGTTTCTTAAGCAACCGCAGTGTATGATATTACTAGC 643
 DB 21553 TGCATTTCACGCGGGTTTCTTTATTCACGCCGAGGAAATGACATTTTCACTGGC 21494
 QY 644 GGGCTGCTTAAGAAAACCGCCGCTGCTAAAGATATTATTCAGTGGCTGGTGAACAAC 703
 DB 21493 GGT-TCCCTTAAGAAAACCGCAGTGAACCGCACTTTTCACTGGCGGTTCCAAATATACC 21435
 QY 704 GCGTGAAGAAAACCGCATTTCTACTAGCCCTAGCTGTGACAGGACATTAATAACGT 763
 DB 21434 GCCAGTG-GAATGCTGATTTTCACTGACCCCTAGC---ACTGGCGGTACTGAAAACCG 21379
 QY 764 CAGTGAAGATAGCTTAGATCTGCTCACTATAGAGTTCTATGACT 809
 DB 21378 CAGTGAAGATAGGTTTGAACCGCCTATAGAGTTCTGTGACT 21333

RESULT 15
 AC146809 133080 bp DNA linear HTG 26-NOV-2003
 LOCUS Zea mays clone ZMMBB0355F08, *** SEQUENCING IN PROGRESS ***, 5
 DEFINITION unordered pieces.

ACCESSION AC146809.2 GI:38348713
 VERSION HTG, HTGS_PHASE1; HTGS_FUILLTOP; HTGS_ACTIVEFIN.
 KEYWORDS Zea mays
 SOURCE Zea mays
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE AUTHORS Birren,B., Nusbaum,C., Lander,E., Butler,E., Wing,R., Bhatti,A.K. and Messing,J.
 TITLE Zea mays, clone ZMMBB0355F08
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 133080)
 AUTHORS Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N., Anderson,M., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhalter,B., Camarata,J., Chang,J., Choepel,Y., Collamore,A., Cook,A., Cooke,P., Cornu,B., DeArrelino,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Fero,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B., Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamet,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., Lui,X., Mabbitt,R., MacLean,C., MacDonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M., McDormid,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Rachupka,A., Ramsamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schupack,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M., Talamae,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X., Wymann,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE Direct Submission
 JOURNAL Submitted (08-OCT-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 REFERENCE 3 (bases 1 to 133080)
 AUTHORS Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N., Anderson,M., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhalter,B., Camarata,J., Chang,J., Choepel,Y., Collamore,A., Cook,A., Cooke,P., Cornu,B., DeArrelino,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Fero,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B., Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamet,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., Lui,X., Mabbitt,R., MacLean,C., MacDonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M., McDormid,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Rachupka,A., Ramsamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schupack,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M., Talamae,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X., Wymann,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE JOURNAL
 COMMENT Submitted (26-NOV-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Nov 16, 2003 this sequence version replaced gi:37574225.
 All repeats were identified using RepeatMasker:
 Smit,A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu

 Bhatti, AK and Messing, J.: The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers, The State University of New Jersey, 190 Frelinghuysen Road, Piscataway, NJ 08854, USA
 (http://pgr.rutgers.edu)
 Butler, E and Wing, R: Arizona Genomics Institute, Biological Sciences West, 448A, P.O. Box 210088, University of Arizona, Tucson, AZ 85721, USA (http://www.genome.arizona.edu)

 Project Information
 Center project name: L29774
 Center clone name: 355_F_8

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 5 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 83985: contig of 83985 bp in length
 83986 84085: gap of 100 bp
 * 84086 119445: contig of 35160 bp in length
 * 119446 119545: gap of 100 bp
 * 119546 128391: contig of 8846 bp in length
 * 128392 128491: gap of 100 bp
 * 128492 130558: contig of 2067 bp in length
 * 130559 130658: gap of 100 bp
 * 130659 133080: contig of 2422 bp in length.

FEATURES
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 /organism="Zea mays"
 /mol_type="genomic DNA"
 /cultivar="B73"
 /sub_species="mays"
 /db_xref="taxon:4577"
 /clone="ZMMBB0355F08"
 /clone_lib="CUGI HindIII BAC library"

ORIGIN
 Query Match 7.1%; Score 88; DB 2; Length 133080;
 Best Local Similarity 65.4%; Pred. No. 1.4e-09;
 Matches 191; Conservative 0; Mismatches 95; Indels 6; Gaps 4;

QY 518 GAACTTAAACCGTATGAGACAAACATTTTCATAGTGTGTTTAAGTACCGGTAG 577
 DB 77810 GAAATTTTAAAAAAGCGGGAACCTTCCACTGCGCACTTAATAAACAACCGCGAG 77751
 QY 578 TGATAATAATATTTTTCACATGCGGTTTCTTAAGCAACCGCAGTGTAAATATATTAC 637
 DB 77750 TGGAAATAGCATTTTCAC-TGGGTTTCTTAATAAACCAGGGAAGTAATAGCATTTTC 77692

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CC vector. The invention are useful for controlling the expression of
CC endogenous as well as exogenous products in a seed-preferred manner. The
CC present sequence is maize j1p1 promoter DNA

XX Sequence 1247 BP; 400 A; 240 C; 249 G; 358 T; 0 U; 0 Other;

Query Match 100.0%; Score 1247; DB 6; Length 1247;
Best Local Similarity 100.0%; Pred. No. 3.2e-295;
Matches 1247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 301 AAGGTGATGTTGAATGACCTAGAGCTAAATAGTTAGCTAAATTTAGTTGAGACATT 360
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DB 601 GTTCTTAAGCAAAACGCGAGTGTCTAATATTTTCACTAGCGGCGCTGAAGAAAAC 660
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QY 781 GGATCGTCACTAAGAGCTTCTATGTACTAGTGTGAACCTGATTTGTATGTGACCA 840
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DB 901 CGATTTCTATAGTATGTTTGTGCAAGCCGAAATAGAAATTAACATTTGCTGTGACAG 960

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QY 961 AAATCCACATTATCATCAAGTTCATGCGCGCCGACAGTACCATCCACGCGTGCCTG 1020
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QY 1021 CGGAGACACGCTGTTGGCTGACCGGACATTTGGCCGATTCAGACATGACACAGCCGAG 1080
DB 1021 CGGAGACACGCTGTTGGCTGACCGGACATTTGGCCGATTCAGACATGACACAGCCGAG 1080
QY 1081 ATAGAAGAAAGACGACGACGCGCGGACCGCGAGTAGTGCATGTCACGCTAGC 1140
DB 1081 ATAGAAGAAAGACGACGACGCGCGGACCGCGAGTAGTGCATGTCACGCTAGC 1140
QY 1141 TGTAGCTTTTTCAGAGCGCTGCTGTAAATACGTAGCCCTTCCACAAAGCGGAGG 1200
DB 1141 TGTAGCTTTTTCAGAGCGCTGCTGTAAATACGTAGCCCTTCCACAAAGCGGAGG 1200
QY 1201 GGGAGAGATATCTGCTAGTACAGAGAGAGTGGCTAGAACTAGCA 1247
DB 1201 GGGAGAGATATCTGCTAGTACAGAGAGAGTGGCTAGAACTAGCA 1247

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RESULT 2

```

ABN85030
ID ABN85030 standard; DNA; 3598 BP.
XX
AC ABN85030;
XX
DT 27-SEP-2002 (first entry)
XX
DE Maize DD1-a promoter.
XX
KM Plant; maize; DD1-a; DD1-b; seed transfer zone; transgenic plant;
XX promoter; chromosome 8q; ds.
XX
OS Zea mays.
XX
FH Key Location/Qualifiers
FT TATA_signal 3518..3524
FT /*tag= a
XX
PN WO200236788-A2.
XX
PD 10-MAY-2002.
XX
PF 06-NOV-2001; 2001WO-FR003439.
XX
PR 06-NOV-2000; 2000FR-00014214.
XX
PR 19-DEC-2000; 2000FR-00016602.
XX
PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.
PA (CNRS ) CENT NAT RECH SCI.
PA (ECOL-) ECOLE NORMALE SUPERIEURE DE LYON.
PA (UYLY-) UNIV LYON I BERNARD CLAUDE.
XX
PI Rogowsky P, Magnard J, Perez P;
XX
DR MPI; 2002-519253/55.
XX
PT New DD1-a and DD1-b genes of maize and their regulators, useful for
PT specific control of transgene expression in the transfer zone of grain
PT during development.
XX
PS Claim 2, Fig 5; 140pp; French.
XX
CC The present sequence is the promoter of maize DD1-a gene. The DD1-a and
CC DD1-b genes are expressed specifically in the transfer zone of the seed
CC during development. They are used to prepare transgenic plants,
CC particularly where their regulatory regions are used to control a wide
CC variety of genes of interest, especially genes that improve agronomic,
CC nutritional or industrial quality. The DD1 genes may also be used for
CC recombinant expression of DD1 proteins, overexpression of which may
CC increase quantity and/or quality of metabolites in the ripe grain and

```

CC Improve resistance to various pathogens. The DDI-a gene is located on
 CC maize chromosome 8q
 XX
 SQ Sequence 3598 BP; 1022 A; 738 C; 739 G; 1098 T; 0 U; 1 Other;
 Query Match 9.6%; Score 119.2; DB 6; Length 3598;
 Best Local Similarity 70.9%; Pred. No. 6.5e-19;
 Matches 190; Conservative 0; Mismatches 68; Indels 10; Gaps 2;
 OY 263 CTTAAATCCAGATATTAGTAGAGATGTTAGTATAGAT-TTAGGTGATGTTTGATGCACT 321
 DB 2362 CAACCTCAAGTGTGGGGGAGTTGTGATAGTAGTAGTGGGTGTTTGATGACT 2421
 OY 322 AGAGCTAATAGTTAGTAGCTAAATAGTTGAGACATCAACACCCCTA-----T 372
 DB 2422 AGAGCTAATAGTTAGTAGCTAAATAGTTGAGACATCTAAACACTCTAGTAAATAGTT 2481
 OY 373 CAATATTAGTTATTTTATAGTAATAGTTAATAGTTAGTTATTTATTAAGTAGCT 432
 DB 2482 CAACATTTAGCTATTTTATAGTAATAGTTAATAGTTAGTTAGTTAGTTAGTT 2541
 OY 433 TTTTTCCTAGCAATTTTTCAGCACTAACAACTTGTGTTAGTATTCAAATACCCCT 492
 DB 2542 AATTCCTAGCAAAATTTTTCAGCACTAACAACTTGTGAGTGCATTCACACCCCTAA 2601
 OY 493 AAGCCGTTAAGTATGCTCTTTCTAGAA 520
 DB 2602 AGAAGATGGACACGATCTAGCGGGA 2629
 RESULT 3
 AAQ40763/c
 ID AAQ40763 standard; DNA; 9824 BP.
 XX
 AC AAQ40763;
 XX
 DT 25-MAR-2003 (revised)
 XX
 DT 14-SEP-1993 (first entry)
 XX
 DE Wild-type shrunken-2 gene.
 XX
 KW Wild-type; shrunken-2; Sh-2; gene; plasmid; replication; Bt-2; starch;
 sequencing; ADP-glucose pyrophosphorylase; ADP-GPP; cloning; sucrose;
 brittle-2; ADP-glucose; pyrophosphate; ATP; sh-2; bt-2; hydrolysis;
 glucose-1-phosphate; chain elongation; starch synthetase; homozygous;
 recessive; supersweet; corn; ss.
 XX
 KW Zea mays.
 OS
 XX
 PN WO9309237-A1.
 XX
 PD 13-MAY-1993.
 XX
 PF 04-NOV-1992; 92WO-EP002531.
 XX
 PF 05-NOV-1991; 91US-00791933.
 PR
 XX
 PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
 PA (SANO) SANDOZ PATENT GMBH.
 PA (SANO) SANDOZ LTD.
 XX
 PI Nichols SE, Pauly MH, Sinibaldi RM, Weeks DP, Baker FC;
 PI Duncan ML;
 DR WPI; 1993-167702/20.
 XX
 DR Super-sweet corn plants and seed - have sweet or starchy kernels at
 PT harvest for food or seed, respectively.
 XX
 PS Claim 23; Page 30-36; 49pp; English.
 XX
 CC This sequence represents the wild-type shrunken-2 (Sh-2) gene. The Sh-2
 CC gene contains a sequence which interferes with plasmid replication which

CC caused difficulties in cloning and sequencing the Sh-2 gene. The Sh-2
 CC gene encodes a 60 kD protein which is involved in starch production. The
 CC Sh-2 protein represents two subunits of the four subunit enzyme ADP-
 CC glucose pyrophosphorylase (ADP-GPP). The other two subunits of ADP-GPP
 CC comprise a 55 kD polypeptide encoded by the brittle-2 (Bt-2) gene. ADP-
 CC GPP catalyses the reversible synthesis of ADP-glucose and pyrophosphate
 CC from ATP and glucose-1-phosphate. The reaction is driven by pyrophosphate
 CC hydrolysis. ADP-glucose is the glucosyl donor for starch chain elongation
 CC catalysed by starch synthetase. When either the Sh-2 or Bt-2 gene is
 CC present in the homozygous recessive state (sh-2 or bt-2 respectively) the
 CC 60 kD or 55kD subunits respectively are not synthesised and little or no
 CC functional ADP-GPP is made. Therefore starch synthesis is impaired,
 CC sucrose accumulates to 2-4 times the levels of normal sweet corn and the
 CC result is "supersweet" corn. (updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 SQ Sequence 9824 BP; 2718 A; 1910 C; 1915 G; 3281 T; 0 U; 0 Other;
 Query Match 8.7%; Score 108.4; DB 2; Length 9824;
 Best Local Similarity 75.2%; Pred. No. 4e-16;
 Matches 152; Conservative 0; Mismatches 41; Indels 9; Gaps 1;
 OY 297 GATTAAAGTGATGTTGAATGCACTAGAGCTAATAGTTAGTACCTAAATAGTTGAGA 356
 DB 9541 GACTTAAAGGGGTGTTGAATGCAATAGAGCTAATAGTTAGTTAAATAGTCTGAAGA 9482
 OY 357 CATTCAAAACACCCCTA-----TCAATTATTAGTTATTTTATAGTAATTTAGTTAATG 407
 DB 9481 CATCTAAACAAATATAGCTAATATAGTTACAGCTATATGCTATTTTAAACAAATATGCTAATAG 9422
 OY 408 TTAGTTAGTTATTTTAAAGCTAGCTTTTCTTCTAGCAATTTTTCAGCACTAACAACTT 467
 DB 9421 TTAGCTAGCTATTTTGTAGCTAGCTAATTTTCACGTCAAATTTTGTGCACTAATTAATT 9362
 OY 468 AGTTTATAGTATTCAAATACC 489
 DB 9361 AGCTCTAATGATTTTAAACACC 9340
 RESULT 4
 ACA62291/c
 ID ACA62291 standard; DNA; 925 BP.
 XX
 AC ACA62291;
 XX
 DT 12-AUG-2003 (first entry)
 XX
 DE Maize proteinase inhibitor gene, promoter.
 XX
 KW Maize; ds; promoter; proteinase inhibitor; plant; development;
 developmental pathway; plant defence response; disease resistance.
 XX
 OS Zea mays.
 XX
 PN US2003033632-A1.
 XX
 PD 13-FEB-2003.
 XX
 PF 23-OCT-2001; 2001US-00039836.
 XX
 PF 25-OCT-2000; 2000US-0243167P.
 PR
 XX
 PA (PION-) PIONEER HI-BRED INT INC.
 PA Crane VC, Simmons CR;
 DR WPI; 2003-466274/44.
 XX
 DR New maize proteinase inhibitor-like polypeptide and polynucleotides
 PT useful in expression cassettes for modulating development, developmental
 PT pathways, and plant defense response, and for enhancing disease
 PT resistance in plants.
 XX

PS Claim 7, Page 26; 29pp; English.

XX
CC The invention relates to a new isolated polypeptide comprising: (a) the
CC maize proteinase inhibitor appearing as ABU61637; (b) a sequence encoded
CC by the nucleotide sequence appearing as ACA62290, or by the cDNA insert
CC deposited as Patent Deposit Number not given in the specification; (c) at
CC least 75% identity to ABU61637, where the polypeptide has proteinase
CC inhibitor-like activity; or (d) at least 20 contiguous amino acids of
CC ABU61637. Also included are an isolated nucleic acid molecule
CC (comprising, or having at least 75% sequence identity to or at least 20
CC contiguous nucleotides of ACA62290 encoding ABU61637, or hybridising
CC under stringent conditions in 50% formamide, 1 M NaCl, 1% sodium dodecyl
CC sulphate (SDS) at 37 pluso C and a wash in 0.1% saline sodium citrate
CC (SSC) at 60-65 pluso C to the complement of the above sequences), a DNA
CC construct comprising the nucleic acid molecule operably linked to a
CC promoter that drives expression in the host cell, a vector comprising the
CC DNA construct, a plant cell comprising the vector, a plant having stably
CC incorporated into its genome at least one of the DNA constructs cited
CC above, a method for modulating disease resistance in plant by stably
CC introducing into the genome of the plant at least one of the DNA
CC construct comprising a heterologous promoter active in the plant, a
CC method for modulating the level of a polypeptide in a plant (by
CC introducing into the genome of the plant cell a DNA construct comprising
CC the polynucleotide operably linked to a promoter, culturing the plant
CC cell under plant growing conditions to produce a regenerated plant, and
CC inducing expression of the polynucleotide for a time sufficient to
CC modulate the level of the polypeptide in the plant) and a method for
CC regulating the expression of a nucleotide sequence of interest (by stably
CC incorporating into the genome of a plant cell a nucleotide sequence of
CC interest operably linked to the promoter cited above. The polypeptide,
CC polynucleotides and methods are useful in expression cassettes for
CC modulating development, developmental pathways, and plant defence
CC response, and for enhancing disease resistance in plants. The present
CC sequence represents the promoter from the maize proteinase inhibitor
CC gene which may be used in the DNA constructs cited above for expressing a
CC gene of interest
XX
SQ Sequence 925 BP; 258 A; 178 C; 202 G; 287 T; 0 U; 0 Other;

Query Match 8.4%; Score 104.6; DB 8; Length 925;

Best Local Similarity 79.7%; Pred. No. 1.5e-15; Mismatches 29; Indels 13; Gaps 3;

Matches 165; Conservative 0; Mismatches 29; Indels 13; Gaps 3;
OY 295 TAGATTAAAGTGATGTTGAATGCACTAGAGCTAAATAGTAGTAAATAGTGGGA 354
DB 465 TAGACTTAAGCCATGTTTGAATGCACTAAAGATTAAGTGGTAAATAGTT-CA 407
OY 355 GACATTCAAAACCCCTATC-----AATTATTAGTTATTTTGAATTAATTAGTTAA 404
DB 406 GACATTCAAAACAGCCCACTTAATTAATTAATTAATTAATTTTGGTAAATTAAGTTAA 347
OY 405 TAGTTAGTATGTTATTTATTAAGTAGCTTTTCTTACTAGCAATTTTTCGCCAACAATA 464
DB 346 TAGTTAGGAGTATTTTGTAGCTAGATTAATTTCACTAACAA--TTTTCGCCAATAACT 289
OY 465 ATTAGTTTATGATTAATCAATACCC 491
DB 288 ATTAGTTTATGATTAATCAATACCC 262

RESULT 5

AAV49471/C ID AAV49471 standard; cDNA; 4695 BP.

XX AAV49471;

XX 10-NOV-1998 (first entry)

DE Maize phyase genomic clone P19.14.

XX Maize; phyase; PCR; amplification; primer; probe; hybridisation;
KW transgenic plant; starch; seed; nutrition; cereal; steep liquor; ss.
XX

OS Zea mays.

XX Key Location/Qualifiers

PH prim_transcript 1935..3403

FT /tag= a

FT exon 1935..1947

FT /tag= b

FT exon /number= 1

FT intron 1948..2078

FT /tag= c

FT exon /number= 1

FT exon 2079..3403

FT /tag= d

FT exon /number= 2

FT CDS 2097..3260

FT /tag= e

FT /product= "phyase"

XX FR2751987-A1.

XX 06-FEB-1998.

XX 01-AUG-1996; 96FR-00009734.

XX 01-AUG-1996; 96FR-00009734.

XX 01-AUG-1996; 96FR-00009734.

XX (BIOC-) BIOCEM SA.

XX (INRG) INRA INST NAT RECH AGRONOMIQUE.

XX Perez P, Maugenest S, Lescure AM;

XX WPI; 1998-133139/13.

XX P-PSDB; AAW49696.

XX DNA encoding maize phyase enzyme - useful for producing recombinant

XX phyase or transgenic plants with increased phyase levels.

XX Claim 9; Fig 4; 67pp; French.

XX This sequence represents the sequence of a genomic clone (P19.14)

XX encoding a maize phyase protein. The sequence was isolated from a maize

XX genomic DNA library screened with the phyase cDNA sequence (AAV49470).

XX From 13 clones isolated from the library, 2 classes of clones were

XX obtained based on their restriction maps. This sequence belongs to the

XX class I clones and has been located on the short arm of chromosome 3

XX between loci umc010 and umc026. The phyase sequence can be used to

XX generate transgenic plants for production of a high level of phyase. The

XX phyase, or seeds containing it, are used to extract starch from plant

XX seeds, especially for increasing the nutritive quality of e.g. cereals,

XX and/or to upgrade steep liquors

XX Sequence 4695 BP; 1347 A; 1021 C; 1013 G; 1314 T; 0 U; 0 Other;

Query Match 7.9%; Score 99; DB 2; Length 4695;

Best Local Similarity 71.1%; Pred. No. 6.3e-14; Mismatches 50; Indels 18; Gaps 2;

Matches 167; Conservative 0; Mismatches 50; Indels 18; Gaps 2;

OY 272 AGATTGTTGATGATGTTAGTATGATTAAGTGATGTTGAATGCACTAGAGTAATA 331

DB 1307 AGTAGTCTCGAGGACTAAATGGATTAAGGGTTTATTGAATGCACTAGAGTAATA 1248

OY 332 GTTAGTACCTAAATTAAGTTGGAGACATTCAAACCCCTATCAAT----- 376

DB 1247 GT---TAGCTAAATTAAGCTAGAGACATCAACACCCCTATGCAATATATATAGTTAGC 1191

OY 377 TATTAGTATTTTATGTAATTAAGTTAATGTTAGTATGTTATTAAGCTAGCTTTT 436

DB 1190 TATTAGTATTTTATGTAATTAAGTTAATGTTAGTATGTTATTAAGCTAGCTTTT 1131

OY 437 TTACTAGCAATTTTATGCACTAACTAATTAAGTTAGTTGATGATCAATACCC 491

DB 1130 CTACTAGTATATTTTATGCTAGCTAATTAAGTTAGTTAGTATGATCAATACCC 1076

RESULT 6
ABX89107 ID ABX89107 standard; cDNA, 318 BP.
XX AC
XX ABX89107;
DT 24-APR-2003 (first entry)
DE Corn ear-derived polynucleotide (cpd) #7567.
XX
XX Corn ear-derived polynucleotide; cdp; cDNA library; SATMON022; SATMON023;
KM structural gene; functional gene; regulatory gene;
KM corn ear-specific profile; gene transcription; gene expression;
KM hybrid plant; desirable trait expression; plant breeding program;
KM inheritance; desired characteristic; growth; development;
KM disease resistance; environmental adaptability; quality; yield;
KM multigene trait; plant; gene; ss.
XX
XX Zea mays.
OS
PN US6476212-B1.
PN
PD 05-NOV-2002.
XX
PF 14-MAY-1999; 99US-00313294.
PR 26-MAY-1998; 98US-0086722P.
XX
XX (INCY-) INCYTE GENOMICS INC.
PI Laigudi RV, Ito LY, Sherman BK,
PI WPI; 2003-208840/20.
DR
XX
XX Novel purified corn-ear derived polynucleotide useful as hybridization
PT probe for detecting polynucleotide in sample, and for identifying,
PT evaluating, and altering desired characteristics associated with growth,
PT development.
XX
XX
XX Example; SEQ ID NO 7567; 390pp; English.
PS
CC The present invention relates to the isolation of corn ear-derived
CC polynucleotides (cdps) from the corn (Zea mays) cDNA libraries SATMON022
CC and SATMON023. Some of the cdfs uniquely identify structural, functional,
CC and regulatory genes of corn ear. The polynucleotide sequences are
CC useful for detecting cdfs in a sample, for producing a corn ear-specific
CC profile of gene transcription, for detecting altered gene expression in
CC hybrid or hybrid plants, and for screening several molecules for specific
CC binding to the polynucleotide. The cdfs are useful to identify, isolate,
CC or extend identical or related corn-ear nucleic acid sequences from DNA
CC libraries, and in nucleic acid amplification or hybridization techniques
CC to follow the expression of desirable traits through plant breeding
CC programs. Preferably, the cdfs are used to identify, evaluate, alter, or
CC follow the inheritance of desired characteristics associated with growth
CC and development, disease resistance, environmental adaptability, quality,
CC and yield of corn. The cdfs are also useful as molecular markers for
CC studying inheritance and multigene traits in a plant breeding program.
CC The cdfs are useful for producing purified corn-ear polypeptides by
CC recombinant techniques. They are also useful in diagnostic assays to
CC detect or confirm conditions or diseases associated with abnormal levels
CC of cdp expression. ABX81541-ABX89140 represent corn ear-derived
CC polynucleotides (cdfs) of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/psipsd/Identify.html
XX
SQ Sequence 318 BP; 90 A; 65 C; 54 G; 97 T; 0 U; 12 Other;

OY		372	TCAATTATTAAGTATTTTAAAGTAGTAAAGTAGTATTTTAAAGCTAGC	431
Dd		22	TCAGCATTAACGATTTTTAGTAATAATTGTAATGGTAGCTATTTGTACTACG	81
OY		432	TTTTTTACTTGACAATTTTTTAGCCAACTAACAATTAGTTAGTGTATTCAAATACCC	491
Dd		82	TAATTCACCTAACAA-TTTTNAGNCAACTAATCTATTAGTTCTTAATACATTCAAACCCC	140
OY		492 T 492		
Dd		141 T 141		
RESULT 7				
AAAA51324	ID	AAAA51324 standard; DNA; 13868 BP.		
XXXXXX	AC			
XXXXXX	AAA51324;			
DT	26-SEP-2000	(first entry)		
DE	Z. mays MADS-box protein ZMM14 gene regulatory sequence.			
KW	ZMM14; maize; MIRK-C-type; MADS-box; DNA-binding; upper floret; spikelet;			
KX	inflorescence; grass; chromosome 1; monocotyledon; regulatory region;			
KX	disease resistance; flowering; growth regulator; herbicide; OSMADSI; de.			
OS	Zea mays.			
PN	MO200037488-A2.			
PD	29-JUN-2000.			
PF	20-DEC-1999; 99WO-EP010116.			
PR	21-DEC-1998; 98EP-0012435.			
PR	29-OCT-1999; 99EP-00121591.			
PA	(PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.			
PI	Cacharron J, Theissen G, Delau W, Saedler H;			
PT	WPJ; 2000-452177/39.			
PS	Disclosure; Page 88-91; 93pp; English.			
XX	This is a regulatory region sequence from the maize (Zea mays) ZMM14 gene			
CC	which encodes a MIRK-C-type MADS-box protein. The protein is involved in			
CC	DNA-binding and is expressed in the upper florets of spikelets of grass			
CC	inflorescences. The ZMM8 and ZMM14 genes (see AAA51322-23) map to			
CC	chromosomes 1 and 9, respectively, and are similar to OSMADSI from rice			
CC	(Oryza sativa). The ZMM8 and ZMM14 genes are useful for study of MADS-box			
CC	transgenic plants having altered level or composition of protein(s) in			
CC	the florets of spikelets, for modulating the number of kernels, for			
CC	conferring or improving disease resistance, generating late or early			
CC	flowering, expressing heterologous proteins in the upper florets in the			
CC	spikelets of grass inflorescence, modifying solute partition in florets,			
CC	improving kernel derived products or the expression of enzymes affecting			
CC	any agronomic aspect of the kernel or the whole inflorescence. Compounds			
CC	identified as being activators or inhibitors of genes specifically			
CC	expressed in the spikelets of grass inflorescence may be used as growth			
XX	regulators and/or herbicides			
SQ	Sequence 13868 BP; 4120 A; 2725 C; 2718 G; 4305 T; 0 U; 0 Other;			
Query March	5.0%; Score 62.6; DB 3; Length 13868;			
Best Local Similarity	56.7%; Pred. No. 7.5e-03;			
Matches 160; Conservative	0; Mismatches 111; Indels 11; Gaps 2;			

PS Claim 1; SEQ ID NO 148; 27bp; English.
XX
XX The invention relates to a nucleic acid comprising a sequence of 18
CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with
CC bisulphite, of genes associated with tumour suppression and oncogenes
CC having a sequence taken from 536 (actually 533 since numbers 408, 458 and
CC 500 are missing from the sequence listing) sequences (Ss) and sequences
CC complementary to (Ss). The nucleic acid may be a peptide nucleic acid-
CC oligomer (PNA) of at least 9 nucleotides and may form part of a set of
CC probes for detecting the cytosine methylation state and/or single
CC nucleotide polymorphisms and also to be used in an array for analysing
CC diseases associated with CpG dinucleotides e.g. cancers and tumours. The
CC probes can also be used in a method for ascertaining genetic and/or
CC epigenetic parameters for the diagnosis and/or therapy of existing
CC diseases or the predisposition to specific diseases, by analysing
CC cytosine methylations. The parameters may be compared to another set of
CC genetic and/or epigenetic parameters, the differences serving as basis
CC for diagnosis and/or prognosis events which are disadvantageous to
CC patients. The present sequence is one of the 533 genomic sequences
CC derived from tumour suppressor genes and oncogenes. Sequences with even
CC numbered Seq ID numbers are the complementary sequence of the
CC corresponding odd numbered sequence (e.g. ID 2 and ID1, ID 536 and ID
CC 535, except for those whose partner sequence is missing). Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_sequences
XX
XX Sequence 5689 BP; 1490 A; 207 C; 1277 G; 2707 T; 0 U; 8 Other;
SQ
Query Match 4.7%; Score 58; DB 4; Length 5689;
Best Local Similarity 49.5%; Pred. No. 0.00073;
Matches 145; Conservative 0; Mismatches 148; Indels 0; Gaps 0;
QY 187 TTGCTTTAACTACGACCACTGATTAATCTTTCAGACACATGTTATCTATTG 246
DB 1641 TTGTTTGGTTTATTAATGAATTAATATATTCGATTTTATTTGTTATTTTCG 1700
QY 247 TTGACTTTAATCAATCAATCAAGATTTAGTAGAGATGTTACTATAGTTAAGTG 306
DB 1701 TTTTATTTTATTTTAAATATTTTATTTTATTTTATTTTATTTATTTATTTT 1760
QY 307 AGTTTGAATGACGACGACTAATAGTTAGTCTAAATTTGTCGACATCTCAACA 366
DB 1761 TTTATTTTAAATATTTTATTTATTTTATTTTATTTTATTTTAAATTTTAA 1820
QY 367 CCGTATCAATTAATAGTTATTTTATTAATTAATTAATTAATTAATTAATTA 426
DB 1821 ATTATTTTATTTTAAATATTAATTAATTAATTAATTAATTAATTAATTTT 1880
QY 427 CTAGCTTTTATTAAGCAATTTTTCGCACTCAATTAAGTTTACTGTA 479
DB 1881 TATATTTTATTTTAAATTAATTTTATTTATTTATTTTATTTTATTTA 1933
RESULT 10
ABK28226
ID ABK28226 standard; DNA; 5689 BP.
AC ABK28226;
XX
XX 23-APR-2002 (first entry)
XX
XX DNA transcription associated complementary genomic DNA #50.
DE
XX
XX DNA transcription associated complementary genomic DNA #50.
KM DNA transcription associated complementary genomic DNA #50;
KM PNA: cytosine methylation state; SNP; retroviral infection; gene; de;
KM single nucleotide polymorphism; adenosine deaminase deficiency; cancer;
KM viral infection; Sezary syndrome; haematological disorder; tuberculosis;
KM immunological disorder; Werner syndrome; developmental disorder;
KM psoriasis; Rieger's syndrome; neurological disorder; erythropoiesis;
KM neurodegenerative disorder; Maardenburg syndrome; Niemann-Pick disease;
KM myelodysplastic syndrome; myocardial infarction; hypertension; arthritis;
KM angiodysplasia; congenital heart disease; HDR syndrome; gene therapy;

KM polyglutamine disorder; solid tumour.
XX
XX OS Unidentified.
XX PN WO200192565-A2.
XX
XX PD 06-DEC-2001.
XX
XX PF 06-APR-2001; 2001WO-EP0039973.
XX
XX PR 06-APR-2000; 2000DE-01019058.
XX PR 07-APR-2000; 2000DE-01019173.
XX PR 30-JUN-2000; 2000DE-01032529.
XX PR 01-SEP-2000; 2000DE-01043826.
XX
XX PA (EPIC-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR MPI; 2002-090046/12.
XX
XX PT New nucleic acids or oligomers, useful for diagnosing or treating
XX diseases associated with DNA transcription, e.g. immunological disorders,
XX Werner syndrome, psoriasis, myocardial infarction, solid tumors or
XX cancer.
XX
XX PS Claim 1; SEQ ID NO 100; 32bp; English.
XX
XX The invention relates to a nucleic acid, which comprises a segment of the
XX chemically pretreated DNA of genes associated with DNA transcription from
XX one of 346 sequences, and an oligomer, in particular an oligonucleotide
XX or peptide nucleic acid (PNA)-oligomer that hybridises to or is identical
XX to the chemically pretreated DNA of genes associated with DNA
XX transcription. The set of oligomer probes are useful for detecting the
XX cytosine methylation state and/or single nucleotide polymorphisms (SNPs)
XX in a chemically pretreated genomic DNA. The nucleic acids are useful for
XX diagnosing or treating diseases associated with DNA transcription
XX (particularly with the methylation status), e.g. adenosine deaminase
XX deficiency, viral infection, retroviral infection, Sezary syndrome,
XX haematological disorders, immunological disorders, Werner's syndrome,
XX tuberculosis, developmental disorders, psoriasis, Rieger's syndrome,
XX neurological disorders, neurodegenerative disorders, Maardenburg
XX syndrome, Niemann-Pick disease, myelodysplastic syndrome, myocardial
XX infarction, hypertension, angiodysplasia, erythropoiesis, congenital heart
XX disease, HDR syndrome, arthritis, polyglutamine disorders, solid tumors
XX or cancer. Sequences ABK28127-ABK28472 represent DNA transcription
XX associated genomic DNA molecules of the invention. Note: The sequence
XX data for this patent did not form part of the printed specification but
XX was obtained in electronic format directly from the European Patent
XX Office
SQ Sequence 5689 BP; 1490 A; 207 C; 1277 G; 2707 T; 0 U; 8 Other;
Query Match 4.7%; Score 58; DB 6; Length 5689;
Best Local Similarity 49.5%; Pred. No. 0.00073;
Matches 145; Conservative 0; Mismatches 148; Indels 0; Gaps 0;
QY 187 TTGCTTTAACTACGACCACTGATTAATCTTTCAGACACATGTTATCTATTG 246
DB 1641 TTGTTTGGTTTATTAATGAATTAATATATTCGATTTTATTTGTTATTTTCG 1700
QY 247 TTGACTTTAATCAATCAATCAAGATTTAGTAGAGATGTTACTATAGTTAAGTG 306
DB 1701 TTTTATTTTATTTTAAATATTTTATTTTATTTTATTTTATTTTATTTATTTT 1760
QY 307 AGTTTGAATGACGACGACTAATAGTTAGTCTAAATTTGTCGACATCTCAACA 366
DB 1761 TTTATTTTAAATATTTTATTTATTTTATTTTATTTTATTTTAAATTTTAA 1820
QY 367 CCGTATCAATTAATAGTTATTTTATTAATTAATTAATTAATTAATTAATTA 426
DB 1821 ATTATTTTATTTTAAATATTAATTAATTAATTAATTAATTAATTAATTTT 1880

Qy 427 CTAGCTTTTTTCTAGCAATTTTTTACCAACTACAAATTAGTTTTAGCTA 479
 ||||| | ||||| | | ||||| ||
 Db 1881 TATATTTTTTATTAATAAATTTTTTATATATTATATTTTTTTAATNNTA 1933

RESULT 11

ADA71938 standard; DNA; 2000 BP.

AC ADA71938;
VV

DT 20-NOV-2003 (first entry)
 yy

Rice gene, SEQ ID 5263.

KW Plant; bacterial infection; fungal infection; viral infection; rice;
 YN 2000-03

gene; ds.

Oryza sativa

PN WO2003000898-A1

PD 03-JAN-2003

22-JUN-2001; 2001WO-IB001105.

PR 22-JUN-2001; 2001WO-IB001105.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX

PI	Chang H,	Chen W,	Cooper B,	Glazebrook J,	Golf SA,	Hou Y;
PI	Chang H,	Chen W,	Cooper B,	Glazebrook J,	Golf SA,	Hou Y;

PI Katagiri F, Quan S, Tao Y, Whitcham S, Xie Z, Zhu T, Zou G, XY

DR WPI; 2003-175290/17.

PT identifying at least one gene involved in plant resistance or response to pathogenic infection for conferring resistance or tolerance to a plant to bacterial, fungal or viral infection by determining or detecting plant gene expression.

PS Claim 27; SEQ ID NO 5263; 899bp; English.
....

The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.

SQ Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other;

Query Match 4.5%; Score 56.2; DB 7; Length 2000;

Best Local Similarity 10.7%; Pred. No. 0.0014;

Matches 99; Conservative 404; Mismatches 412; Indels 8; Gaps 3;

Oy	272	AGATATTAGTAGAGTGTAGTATGATTAAGAGTAGTTGAANGCACTAGACATAA	33.1
Db	1053	AAATTAACAACACTTTCTGTGTAGTGAGTGCTKMRRTYTSMSWTYAMMKRYKYM	994
Oy	332	GTTAGTAGCCTAAAATGATGTGAGACATTCAAACCCCTATCAATATTTGTTATTTTA	39.1
Db	993	TAASTFWKMYWYAKMAYAMSRSRKTMMCTGKRATYCGTKMAAAGRMRDMAWCYC	934
Oy	392	GTAATTAATTAATAGTTAGTAGTATTTAATAACCTAGCTTTTTTACTAGAATTTTT	45.1
Db	933	MWKMWKCTSCKMWKTRTWSCWYTWMGAMRAYYAMRRRWTYKWSMRREYWTMTKW	874
Oy	452	TAGCCAACTAACAATTAGTTTAGTGATTTCAAAATACCCTAACCCGTTAAGTAGTGC	51.1

Db 873 TMTCTCAKAKYMTATGATATMMWRRYTTYTYCYANTCAKCKYKMATMTKMTTTCACMRATS 81.4

Qy 512 TTTCTGAATCTTAAACCGTATGTGAGCAACATTTTCATGTGTACTGTTTAAGTCAC 571.1

Db 813 WRRAAAGRMRRYKQKRAYYMWRMWRCKKAGMAMWNRKSRYEMKKYKATRYMGMAMTW 75.4

Oy 572 CGTCACTGATAAATAATTTTCACATGGGTTTCTTAGCAAAGCCGACGTATGAT 631D
::: ::: |::: |::: |::: |::: |::: |:::
Db 753 MMSWRWKSYSRWMSGGRMRSAMPEYCSRMCAKTKVASASRTKRASKSYRARRWYMK 694D

Dy 632 ATTTCACCTAGCGGGCTGCTAAAGAACCCGCCGTCTAAAGATATTTCACCTAGCGGT 691
:: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 693 RKQWTRRYRKYPMSCMTBAPMSKRRKMGASMKSCMMYWRGARSMYSKYSCSAPCKKT 634

692 TGGT-GAACAACCTGCTGTGAAAAAGCCGATTCTACTAGCCCTGACATGGCG 750
 633 RYTTSSYMGTYGMYSSYKMSMTSSKMSYMGKMTCTMYTSSMKSTSRSKGMRGMSRM 574

Dbb QY
751 ACATAAAAAAGCTCAGTGAATAATAGCTTAGAGTCGTACTATAGACGTTCTAATGTAATT 810
::: :: ::: : :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: |
573 YWRMWMKKRKRKYMYMMKMKCTWRCMCYRYNGYTMTYSRSRMNYTORLYAKARYTSKKRYM 514

DQ 811 AGTGGTTAACTAGATATTGTAGTCACCAAGTGCCGCTTTTAATAAACCAACTAAA 870
:
: : : : :
513 WKYKRYCYYTYGNMTMCKSYMMRRGYCKACKCCYAMCMIAAASGMNMYRKYSSMR 454

871 TACTAGTAATAATCTAGTGTGCAATTGCATTTCTATAGTAATGGTTTGCTTCGAAC 930
 : : : : : | : : : : :
 453 MSTRKTMMSMTWKCKCSMRYGAKGCGCCMMYTCGYVKKWTTYNGSFKYSRCRYVMNNM 394

931 CGGAATAGAGTAAACATTTCGTGCA-----CAGAAATCCACATTACATCAAGTTCAT 985
 393 YGAGHATMTATYSYSMTATTTYYATKYKWTYKRGKGTSMWYKSYKTKKCTTWCCTMKCMCR 334

[illegible]

Oy 1046 ACAATTGGCCGATCGACAGCTGCACACACCGACAATTG--MAGAAGAAGCAGCACG 110
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Db 273 YSNKYKKYKMMKKSYNMGARSSGIWSRAAKRTYKGISTSRADOMDPCRMYSACRR 214

1104 CGGCGGACCGCGGAGTAGTGACGCTGACGCTGTTTGGACAGCGTCT 116
 213 YRTSYGCGCSTCGSSKKMYMSKCSMMRTSSSCSCYCTYYAMCSCMSCMNYGSC 154

QY 1164 CTGTAATACGTAGCCCTTCAC 1186
| : : : : : | : : : : : |
nb 153 GCYTRGWRKRSKYSMCKKCSG 131

RESULT 12

ID AAS45309 standard; DNA; 10286 BP.

AC AAS45309;

DT 18-DEC-2001 (first entry)

DE Chemically pretreated complementary DNA associated with cell cycle #7.
 XX
 XX Cell cycle; human; CPG dinucleotide; cytosine methylation; HIV; aging;
 KW human immunodeficiency virus; neurodegenerative disorder; solid tumour;
 KW graft-versus-host disease; glomerular disease; Lewy body disease; cancer;
 KW arthritis; arteriosclerosis; anti-HIV; neuroprotective; antiarrhythmic;
 KW immunosuppressive; antitumour; cytosolatic; antiarteriosclerotic; ds;
 KW PCR primer.

OS	Homo sapiens.
XX	
PN	WO200168911-A2
XX	
PD	20-SEP-2001.

[illegible]

DB	2684	ACNAAAGTAAATTAACATTAATTAAATTTAAATTAATTAAC	2641
RESULT 13			
ID	ABK28148/c		
XX	ABK28148 standard; DNA; 10286 BP.		
AC	ABK28148;		
XX			
DT	23-APR-2002 (first entry)		
XX			
DE	DNA transcription associated complementary genomic DNA #11.		
XX			
KW	DNA transcription associated gene; peptide nucleic acid; PNA-oligomer;		
KW	PNA; cytosine methylation state; SNP; retroviral infection; gene; ds;		
KW	single nucleotide polymorphism; adenosine deaminase deficiency; cancer;		
KW	viral infection; Sezary syndrome; haematological disorder; tuberculosis;		
KW	immunological disorder; Werner syndrome; developmental disorder;		
KW	psoriasis; Rieger's syndrome; neurological disorder; erythropoiesis;		
KW	neurodegenerative disorder; Waardenburg syndrome; Niemann-Pick disease;		
KW	myelodysplastic syndrome; myocardial infarction; hypertension; arthritis;		
KW	angiogenesis; congenital heart disease; HDR syndrome; gene therapy;		
KW	polyglutamine disorder; solid tumour.		
XX			
OS	Unidentified.		
XX			
PN	WO200192565-A2.		
XX			
PD	06-DEC-2001.		
XX			
PF	06-APR-2001; 2001MO-EP003973.		
XX			
PR	06-APR-2000; 2000DE-01019058.		
PR	07-APR-2000; 2000DE-01019173.		
PR	30-JUN-2000; 2000DE-01032529.		
PR	01-SEP-2000; 2000DE-01043826.		
XX			
PA	(EPIG-) EPIGENOMICS AG.		
XX			
PI	Olek A, Plegenbrock C, Berlin K;		
XX			
DR	WPI; 2002-090046/12.		
XX			
PT	New nucleic acids or oligomers, useful for diagnosing or treating		
PT	diseases associated with DNA transcription, e.g. immunological disorders,		
PT	Werner syndrome, psoriasis, myocardial infarction, solid tumors or		
PT	cancer.		
XX			
PS	Claim 1; SEQ ID NO 22; 32pp; English.		
XX			
XX	The invention relates to a nucleic acid, which comprises a segment of the		
CC	chemically pretreated DNA of genes associated with DNA transcription from		
CC	one of 346 sequences, and an oligomer, in particular an oligonucleotide		
CC	or peptide nucleic acid (PNA)-oligomer that hybridises to or is identical		
CC	to the chemically pretreated DNA of genes associated with DNA		
CC	transcription. The set of oligomer probes are useful for detecting the		
CC	cytosine methylation state and/or single nucleotide polymorphisms (SNPs)		
CC	in a chemically pretreated genomic DNA. The nucleic acids are useful for		
CC	diagnosing or treating diseases associated with DNA transcription		
CC	(particularly with the methylation status), e.g. adenosine deaminase		
CC	deficiency, viral infection, retroviral infection, Sezary syndrome,		
CC	haematological disorders, immunological disorders, Werner syndrome,		
CC	tuberculosis, developmental disorders, psoriasis, Rieger's syndrome,		
CC	neurological disorders, neurodegenerative disorders, Waardenburg		
CC	syndrome, Niemann-Pick disease, myelodysplastic syndrome, myocardial		
CC	infarction, hypertension, angiogenesis, erythropoiesis, congenital heart		
CC	disease, HDR syndrome, arthritis, polyglutamine disorders, solid tumours		
CC	or cancer. Sequences ABK28127-ABK28472 represent DNA transcription		
CC	associated genomic DNA molecules of the invention. Note: The sequence		
CC	data for this patent did not form part of the printed specification but		
CC	was obtained in electronic format directly from the European Patent		
CC	Office		
XX			

PR 07-APR-2000; 2000DE-01019173.
PR 30-JUN-2000; 2000DE-01032529.
PR 01-SEP-2000; 2000DE-01043826.
XX
XX (EPIC-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2002-010834/01.
XX
XX New nucleic acid, useful for diagnosis and therapy of metabolic disease,
PT solid tumor and cancers, comprises segment of chemically modified genomic
PT sequences of genes associated with metabolism.
PS
PS Claim 1; Page 64-65; 143pp; English.
XX
XX The invention relates to a nucleic acid (I) comprising a sequence at
CC least 18 bases of a segment of the chemically pretreated DNA of genes
CC associated with metabolism such as DUSP2 (NM_004418), EPHX2 (NM_001979),
CC ODPK (NM_000320), SCSH (NM_000199), SHMT2 (NM_005412), SLC7A2
CC (NM_003046), SLC7A4 (NM_004173) and TYMS (NM_001071) (all undefined). (I)
CC are useful for diagnosis and therapy of metabolic disease, solid tumours
CC and cancers; as primer oligonucleotides for the amplification of DNA
CC sequences, for detecting the cytosine methylation state and/or single
CC nucleotide polymorphisms (SNPs) in a chemically treated DNA of genes
CC associated with metabolism. An array of (I) is useful for ascertaining
CC genetic and/or epigenetic parameters for the diagnosis and/or therapy of
CC existing diseases or the predisposition to specific diseases by analysing
CC cytosine methylations. The method involves chemically treating genomic
CC DNA sample by a solution of bisulphite, hydrogen sulphite or disulphite
CC such that cytosine bases which are unmethylated at the 5th-position are
CC converted to uracil or another base which is dissimilar to cytosine in
CC terms of hybridisation behaviour and amplifying fragments of the
CC chemically pretreated genomic DNA. The genomic DNA is from cells or
CC cellular components which contain DNA, sources of DNA comprising, for
CC e.g. cell lines, biopsies, blood, sputum, stool, urine, cerebral-spinal
CC fluid, tissue embedded in paraffin such as tissue from eye, intestine,
CC kidney, brain, heart, prostate, lung, breast or liver, histologic object
CC slides and their combinations. Genetic parameters are mutations, in
CC particular insertions, deletions, point mutations, inversions and
CC polymorphisms of genes associated with metabolism and sequences further
CC required for their regulation. Epigenetic parameters are in particular
CC cytosine methylations and further chemical modifications of DNA bases of
CC genes associated with metabolism. Further epigenetic parameters include
CC for e.g. the acetylation of histones which correlates with DNA
CC methylation. AAS53306-AAS63373 represent chemically pretreated metabolism
CC associated genes, and related primers of the invention
XX
XX
SQ Sequence 6219 BP; 1714 A; 141 C; 1278 G; 3086 T; 0 U; 0 Other;
Query Match 4.4%; Score 55.2; DB 6; Length 6219;
Best Local Similarity 51.0%; Pred. No. 0.0037;
Matches 155; Conservative 0; Mismatches 148; Indels 1; Gaps 1;
QY 150 TCAGCAGTGGTTGATAGGTTTAACGATCTAATATCTTGTCTTAATACTACCAAC 209
DB 2150 TTAGATTTTGTATTGTTGGTTCGCTTTTATATTTAATAGTTTCTTTTGAAGTTT 2209
QY 210 TGATTAATATCTTTCGACACATGTTAATATCTATTTGACTTAAATCAATACTAATC 269
DB 2210 TTATTAATATTTTATTAATTAAGGTTAAAGTAAATTAATTAAGTAAGTATTAATTT 2269
QY 270 CAAGATTAATAGAGATGTTAGTAAGATTAAAGTATGATGTTGAATGCACTAGACTAA 329
DB 2270 AAAAATAAATGAAGATAGTTAGTTTATTAGGAAAGTTTATGAGAGGTGTTGAA 2329
QY 330 TAGTAGTAGCAATAATAGTTGAGACATTCACACACCCATCAATATTAGTATTTT 389
DB 2330 TTTATTTTGGTATTAGTAGGGGTGTTGTTGATGAAATTTGA-AATTAATTTTATTAATTT 2388
QY 390 TAGTAATTAATAGTTAATAGTTAGTTAATTTAATAGCTAGCTTTTCTAGCAATTT 449
DB 2389 GGGGAAATTTTGAATTTGTAGTTAGATTTTCTAGGGGTTATATGAGAGATTAA 2448

QY 450 TTTA 453
DB 2449 TTTA 2452

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OM nucleic - nucleic search, using sw model

Run on: July 17, 2004, 12:19:35 ; Search time 85 Seconds
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Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

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Listing first 45 summaries

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	102.6	8.2	4137	3	US-08-750-357-7 Sequence 7, Appl1
C 2	78.2	6.3	318	4	US-09-313-294A-7567 Sequence 7567, Ap
C 3	46.8	3.8	640681	4	US-09-790-988-1 Sequence 1, Appl1
C 4	45.8	3.7	8093	4	US-10-204-708-32 Sequence 32, Appl1
C 5	44.6	3.6	20674	4	US-09-641-638-651 Sequence 651, App
C 6	44.4	3.6	5152	4	US-10-204-708-73 Sequence 73, Appl1
C 7	44.2	3.5	6306	4	US-10-204-708-49 Sequence 49, Appl1
C 8	43	3.4	6768	1	US-08-107-755A-1 Sequence 1, Appl1
C 9	43	3.4	8457	1	US-07-991-867B-1 Sequence 1, Appl1
C 10	43	3.4	8457	2	US-08-544-332-1 Sequence 1, Appl1
C 11	43	3.4	8457	4	US-09-370-861A-1 Sequence 1, Appl1
C 12	42.8	3.4	1664976	4	US-08-916-421B-1 Sequence 1, Appl1
C 13	42.6	3.4	7015	3	US-09-177-249-6 Sequence 6, Appl1
C 14	42	3.4	4539	1	US-08-119-512-1 Sequence 1, Appl1
C 15	42	3.4	4539	1	US-08-488-015B-1 Sequence 1, Appl1
C 16	42	3.4	4542	3	US-08-814-412-11 Sequence 11, Appl1
C 17	41.4	3.3	1431	3	US-09-316-083-2 Sequence 2, Appl1
C 18	41.4	3.3	1431	4	US-09-933-700-2 Sequence 2, Appl1
C 19	41.4	3.3	5666	4	US-10-204-708-30 Sequence 30, Appl1
C 20	41.2	3.3	20674	4	US-09-641-638-651 Sequence 651, App
C 21	41.2	3.3	58407	4	US-08-916-421B-2 Sequence 2, Appl1
C 22	41	3.3	19124	2	US-08-487-825B-13 Sequence 13, Appl1
C 23	41	3.3	1664976	4	US-08-916-421B-1 Sequence 1, Appl1
C 24	40.8	3.3	1079	1	US-07-781-355-1 Sequence 1, Appl1
C 25	40.6	3.3	6317	4	US-10-204-708-11 Sequence 11, Appl1
C 26	40.6	3.3	11049	4	US-10-204-708-21 Sequence 21, Appl1
C 27	40.4	3.2	615	3	US-08-998-416-186 Sequence 186, App

C 28	40.4	3.2	636	3	US-08-998-416-1137 Sequence 1137, Ap
C 29	40.4	3.2	636	3	US-08-998-416-1137 Sequence 1137, Ap
C 30	40.4	3.2	837	3	US-08-998-416-288 Sequence 288, App
C 31	40.4	3.2	5152	4	US-10-204-708-74 Sequence 74, Appl1
C 32	40	3.2	1609	3	US-09-377-648-1 Sequence 1, Appl1
C 33	40	3.2	6156	4	US-10-204-708-60 Sequence 60, Appl1
C 34	39.8	3.2	2334	1	US-08-062-632-4 Sequence 4, Appl1
C 35	39.6	3.2	6306	4	US-10-204-708-50 Sequence 50, Appl1
C 36	39.6	3.2	6583	4	US-10-204-708-26 Sequence 26, Appl1
C 37	39.6	3.2	10640	4	US-09-417-485D-5 Sequence 5, Appl1
C 38	39.4	3.2	1887	4	US-09-601-198-39 Sequence 39, Appl1
C 39	39.4	3.2	3095	6	US-09-790-988-1 Patent No. 5231168
C 40	39.4	3.2	640681	4	US-09-790-988-1 Sequence 1, Appl1
C 41	39.2	3.1	832	4	US-09-621-976-2813 Sequence 2813, Ap
C 42	39.2	3.1	11049	4	US-10-204-708-22 Sequence 22, Appl1
C 43	39	3.1	19233	4	US-10-204-708-45 Sequence 45, Appl1
C 44	38.8	3.1	828	3	US-08-998-416-538 Sequence 538, App
C 45	38.6	3.1	615	3	US-08-998-416-186 Sequence 186, App

ALIGNMENTS

RESULT 1
US-08-750-357-7/C
; Sequence 7, Application US/08750357
; Patent No. 6008437
; GENERAL INFORMATION:
; APPLICANT: KREBBERS, Enno
; APPLICANT: WILLIAMS, Mark
; APPLICANT: LEMANS, Jan
; TITLE OF INVENTION: USE OF ANTHOCYANIN GENES TO MAINTAIN
; TITLE OF INVENTION: MALE STERILE PLANTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22131-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,357
; FILING DATE: 21-MAR-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 018030-100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4137 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli region of plasmid pCOL13
; FEATURE:
; NAME/KEY: prim_transcript
; LOCATION: 188
; NAME/KEY: exon
; LOCATION: 188..212
; FEATURE:
; NAME/KEY: 188..212
; LOCATION: 188..212
; FEATURE:

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NAME/KEY: intron
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OTHER INFORMATION: This exon continues up to the polyadenylation site."
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NAME/KEY: CDS
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LOCATION: 1269..2771
OTHER INFORMATION: /note= "Fragment of B-peru coding
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FEATURE:
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? OS=08-750-357-7

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Matches 151; Conservative	0;	Mismatches 49;	Indels 9;	Gaps 1;

Qy	Db	Qy	Db
295	3537	355	3477
TAGATTAGAGTGATGTTGGAATGACATAGAGCTAATGTTAGTACGCAAAAATTGGTGG	TTGACTAAGGGGTGTTGTTAGTATCACTAGAACATATATGATCTGCTAAAAATTGAGTGA	GACACTTCAAAACCCCTA-----TCAAATATATAGTTATTTTATAGTAAATTGTTAAT	GACTTCAAAACAAATATAGCTAATATATTTGATAGCTATTTAGCTACTTTTGACAAATTAGCTAAT
354	3478	405	3418

Oy 406 AGTAGTAGTAGTAATTATTAAGCTAGCTTTTTTTACACCAATTTTTCGCCAATAACCA 465
 Db 3417 ATTAGCTAGCTAATTATTAACCACTAATTTTAAATTTTAAACCACTAATACTA 3358

Qy	466	TTAGTTTACGTATTCAATACCCCTAA	494
Db	3357	TTAGTTCAGTACATTAAACACCTTAA	3329

RESULT 2
US-09-313-294A-7567

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; sequence /56/, Application US/093
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.

```

APPLICANT: Sherman, Bradley K.
 TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
 FILE REFERENCE: PL-0017 US
 CURRENT APPLICATION NUMBER: US/09/313 264A

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; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 7567

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; LENGTH: 318
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:

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OTHER INFORMATION: Incyte ID No. 6476212 700381949H1
NAME/KEY: unsure
LOCATION: 101, 104, 234, 255, 258, 268, 280, 285-286, 289, 297, 314
OTHER INFORMATION: a t c g or other

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				Gaps 1

QY	372	TCGAATTATTAGTATTTTGTAGTAAATTGTTAAATAGTATGTTATTTATTAAGCTAGC	431
	22	TCAGCTATTAGTATTTTGTAGTAAATTAGTTAAATAGTATGATGACGCTATTTGTATGCTAGC	81
QY	432	TTTTTTTACTAGCAATTTTTTAGCCCACTAACAAATTAGTTTGTATTTCAATAATCCC	491
	82	TAAATTCACATTAACA- TTTTATGACCACTAACCTATTTGTCTTATATACATTTCAACACCCC	140

QY	492 T	492
Db	141 T	141

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RESULT 3
US-09-790-988-1/c
; Sequence 1, Application US/09790988
; Patent No. 6632935
; GENERAL INFORMATION:
; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: WATANABE, HIDEKI
; APPLICANT: HATTORI, MASAHIRA
; APPLICANT: SAKAKI, YOSHIYUKI
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
; FILE REFERENCE: 081356/0159
; CURRENT APPLICATION NUMBER: US/09/790,988
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP2000-107160
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera sp.
US-09-790-988-1

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Best Local Similarity 47.1%; Pred. No. 0.071;
Matches 144; Conservative 0; Mismatches 162; Indels 0; Gaps 0;

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DB 268417 AAATATTAACAATAAATATGATCTTTATTTTAAAAAATATCATATTTATGTAAT 268358

QY 223 TCGACACATGTTATATCTATTTGACTTAAATCAATCAATCCAGATATTAGTA 282
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QY 283 GAGATGTTAGTATGATTAAGTGAATGTTGAATGACATAGAGCTAATAGTAGTGA 342
DB 268297 AAGATCTTATCTATATAGTAATTAATTAATTTACTATGCAAAAAAATTTTAAACATA 268238

QY 343 AAATTAGTTGAGACATCAACACCCCTATCAATTAATTTTATTTTAAATTTAGT 402
DB 268237 CAATCTATTTTAAATAAAAAATTTTATTTTGAAGCTTTAAAGATCTTACAAGTC 268178

QY 403 AATAGTATGTTAGTATTTATTAAGCTAGCTTTTCTTACTAGCAATTTTACCAACTAA 462
DB 268177 AATATTATTTATCAACTTCAAAAGACATCCCTAGACGCAAAAAATTTATGTCATCAAC 268118

QY 463 CAATTA 468
DB 268117 TAAATGA 268112

RESULT 4
US-10-204-708-32
; Sequence 32, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PISENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
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; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 32
; LENGTH: 8093
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-32

Query Match      3.7%; Score 45.8; DB 4; Length 8093;
Best Local Similarity 48.1%; Pred. No. 0.02;
Matches 163; Conservative 0; Mismatches 172; Indels 4; Gaps 1;

QY 214 AATAATCTTTGACACATGTTATTTATCTATTTGACTTTAATCAATCAATTCAG 273
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QY 274 ATATTAGTAGACATCTTAGTATAGATTAAAGTGATTTGAATGACATGACTAATGT 333
DB 1894 AATAATAAGTTATGTTGTTTGTAA- - -TTTATTTTAATATAGTAATAATAAAGT 1949

QY 334 TAGTAGCTAAATTTAGTTGAGACATTCACACCCCTATCAATTTATTTAGTTAGT 393
DB 1950 TAGTTGTTATTTGTTTGTCTATTTATTTATTAAGTGAAGAAAGAAATATTTAGT 2009

QY 394 AAATTAGTTAATAGTTAGTTAGTTATTTAATAAGCTATTTTCTTACTAGCAATTTTGA 453
DB 2010 TTTTGTATTTTATTTATTTATTTTAAATTTTATTTTATTTTATTTTATTTTATTTT 2069

QY 454 GCCACTAACAATTTGTTTATGTTATTTCAATTAACCCCTAAGCCCTAAGTATGCTCT 513
DB 2070 TTTATGTTTATTTTATTTTATTTTATTTTGAATAGTTAATTTTATTAATAAATTTT 2129

QY 514 TCTAGATCTTAAACCTATGTCGAGACAAATTTTCATA 552
DB 2130 AGAAATTTATTTATTTTAAATTTGAAGTATTTTATTTT 2168

RESULT 5
US-09-641-638-651/c
; Sequence 651, Application US/09641638
; Patent No. 6432648
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Chumakov, Ilya
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
; FILE REFERENCE: GENSET.051CP1
; CURRENT APPLICATION NUMBER: US/09/641,638
; CURRENT FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 651
; LENGTH: 20674
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1123-..3123
; OTHER INFORMATION: 5' regulatory region
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NAME/KEY: exon
LOCATION: 3124..3297
OTHER INFORMATION: exon 1
NAME/KEY: exon
LOCATION: 3871..4072
OTHER INFORMATION: exon 2
NAME/KEY: exon
LOCATION: 5552..5563
OTHER INFORMATION: exon 3
NAME/KEY: exon
LOCATION: 5758..5880
OTHER INFORMATION: exon 4
NAME/KEY: exon
LOCATION: 5996..6099
OTHER INFORMATION: exon 5
NAME/KEY: exon
LOCATION: 6349..6509
OTHER INFORMATION: exon 6
NAME/KEY: exon
LOCATION: 7379..7522
OTHER INFORMATION: exon 7
NAME/KEY: exon
LOCATION: 8645..8854
OTHER INFORMATION: exon 8
NAME/KEY: exon
LOCATION: 12254..12340
OTHER INFORMATION: exon 9
NAME/KEY: exon
LOCATION: 12854..13023
OTHER INFORMATION: exon 10
NAME/KEY: exon
LOCATION: 13308..13429
OTHER INFORMATION: exon 11
NAME/KEY: exon
LOCATION: 16567..16667
OTHER INFORMATION: exon 12
NAME/KEY: exon
LOCATION: 16775..16945
OTHER INFORMATION: exon 13
NAME/KEY: exon
LOCATION: 17063..17554
OTHER INFORMATION: exon 14
NAME/KEY: misc_feature
LOCATION: 17555..20674
OTHER INFORMATION: 3'regulatory region
NAME/KEY: allele
LOCATION: 1128
OTHER INFORMATION: 10-508-191 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 1182
OTHER INFORMATION: 10-508-245 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 1559
OTHER INFORMATION: 10-509-284 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 1570
OTHER INFORMATION: 10-509-295 : deletion of C
NAME/KEY: allele
LOCATION: 1827
OTHER INFORMATION: 10-510-173 : variable motif ATTTA or TTTTT
NAME/KEY: allele
LOCATION: 2048
OTHER INFORMATION: 10-511-62 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 2323
OTHER INFORMATION: 10-511-337 : insertion of T
NAME/KEY: allele
LOCATION: 2341
OTHER INFORMATION: 10-512-36 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 2623
OTHER INFORMATION: 10-512-318 : polymorphic base A or G
NAME/KEY: allele

LOCATION: 2832
OTHER INFORMATION: 10-513-250 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 2844
OTHER INFORMATION: 10-513-262 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 2934
OTHER INFORMATION: 10-513-352 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 2947
OTHER INFORMATION: 10-513-365 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 3802
OTHER INFORMATION: 12-206-81 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 4062
OTHER INFORMATION: 10-343-231 : deletion of C
NAME/KEY: allele
LOCATION: 4088
OTHER INFORMATION: 12-206-366 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 4109
OTHER INFORMATION: 10-343-278 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 4170
OTHER INFORMATION: 10-343-339 : polymorphic base G or T
NAME/KEY: allele
LOCATION: 5903
OTHER INFORMATION: 10-346-23 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6019
OTHER INFORMATION: 10-346-141 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6141
OTHER INFORMATION: 10-346-263 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 6183
OTHER INFORMATION: 10-346-305 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 6338
OTHER INFORMATION: 10-347-74 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6375
OTHER INFORMATION: 10-347-111 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 6429
OTHER INFORMATION: 10-347-165 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 6467
OTHER INFORMATION: 10-347-203 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6484
OTHER INFORMATION: 10-347-220 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6534
OTHER INFORMATION: 10-347-271 : polymorphic base A or T
NAME/KEY: allele
LOCATION: 6611
OTHER INFORMATION: 10-347-348 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 7668
OTHER INFORMATION: 10-348-391 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 8608
OTHER INFORMATION: 10-349-47 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 8658
OTHER INFORMATION: 10-349-97 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 8703
OTHER INFORMATION: 10-349-142 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 8777


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CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2003-05-06
PRIORITY APPLICATION NUMBER: PCT/EP01/03971
PRIORITY FILING DATE: 2001-04-06
PRIORITY APPLICATION NUMBER: DE 10019058.8
PRIORITY FILING DATE: 2000-04-06
PRIORITY APPLICATION NUMBER: DE 10019173.8
PRIORITY FILING DATE: 2000-04-07
PRIORITY APPLICATION NUMBER: DE 10032529.7
PRIORITY FILING DATE: 2000-06-30
PRIORITY APPLICATION NUMBER: DE 10043826.1
PRIORITY FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 73
LENGTH: 5152
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-73

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Query Match	3.6%;	Score 44.4;	DB 4;	Length 5152;
Best Local Similarity	46.0%;	Pred. No. 0.04;		
Matches 185;	Conservative 0;	Mismatches 216;	Indels 1;	Gaps 1.

Qy	52	CAATTATATTTAAAAACCTAAAAAAAACCTTTATCACCGTACGGAGAGAGATCAACT	111
Db	4014	CAAAAAAAAAAAAAAAAAAAAAAAAAATTTAAACATATAATATACACGCCATCATAT	3955
Qy	112	TGCTATTAGTTTATATGACATTTAAACACCCTTGCAGACATCGACAGTGGTTGATAGTTTA	171
Db	3954	AACATATTATATATCTTATATATTTAAAAAAATCTTTAAATTTTATATTTTATTTTAT	3895
Qy	172	ACGTATATCTAATATCTGTCTTTAATACATGACCA-ACGTATATATATCTTTGCAACAC	230
Db	3894	TTTTTAAATTTTAACTTATTTTAAATTTAAATTTCAAAAAATATATATACAAATTTATTACCGAAC	3835
Qy	231	ATGTTATTATCTATGTTGACTTAAATCAATACAAATCCAGATATATAGTAGAGATGTT	290
Db	3834	ATTAATATCAATTTTCTTTAAACCTTAAAAATTTAAAAAATATTTTTCATTTAAACT	3775
Qy	291	AGTATAGATTAAAGTGATGTTTGAATGCATGACGTAAATGTTAGTACGTAAATTAGT	350
Db	3774	AATTTCTTTAAGCATCTTTTATTTATAAAAAATTTTCCATCTTTTAAAAAAAATTTCT	3715
Qy	351	TGGAGACATTCAAACACCTATCAATATATATGTTATTTTAGTAATATAGTTAATAGTTA	410
Db	3714	AAATATCTTAATATTTAAAAAACACTCTTACACTATAATATTTCTTAATTTCTTACAAACTAT	3655
Qy	411	GTTAGTATTTATATAGTACTTTTTTTATCTAGCAATTTT	452
Db	3654	ATTTTACTTATTTCTTTACATTTTACAAAAAATCAAAATTTT	3613

RESULT 7
US-10-204-708-49
Sequence 49, Application US/10204708
Patent No. 6677731
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: by Assessing DNA Methylation
FILE REFERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/204, 708
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: PCT/EP01/03971
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019958.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07

```
/ PRIOR APPLICATION NUMBER: DE 10032529.7
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: DE 10043826.1
/ PRIOR FILING DATE: 2000-09-01
/ NUMBER OF SEQ ID NOS: 98
/ SEQ ID NO 49
/ LENGTH: 6306
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-49

Query Match      3.5%; Score 44.2; DB 4; Length 6306;
Best Local Similarity 47.1%; Pred. No. 0.049;
Matches 136; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

QY 178 ACTAATCTGCTCTTAATACGACCACTGATTAATCTTCGAACATCTTAT 237
DB 2545 AATTAATATTTATTTAGTAACTGTTGATGTGTGATTAATTAATTAAGTTTAA 2604
QY 238 TATCTATGCTGCTTAACTAATCAATCAAGATATAGTAGATGTTAGTATAG 297
DB 2605 AGTTTAATTAATTAATTTAAGATAGTGTATTTATGCTGTAGTAGAGGTTTAT 2664
QY 298 ATTAAGTATGTTTGAATGACATAGAGCTAATAGTATAGCTAAATTAAGTTGAGAC 357
DB 2665 GGGAGAGTAAATGTTAAATTTATGTAATGTTAAAGTTTATTTTAAAGTTTAA 2724
QY 358 ATTCAACACCCATCAATTAATTTAGTATTTTAAATTAAGTATAGTATAGTAT 417
DB 2725 TGAATAGTTTAAATGATTAATTTATTTTAAATTAATTAATTAATTAATTAAT 2784
QY 418 ATTATAGCTAGCTTTTCTTACGAACTTTTGAACCACTAACAAT 466
DB 2785 TTTTGTATATATATGATTTTATTAATTAATTTAAGTATTAATTAAT 2833

RESULT 8
US-08-107-755A-1/c
/ Sequence 1, Application US/08107755A
/ Patent No. 5721352
/ GENERAL INFORMATION:
/ APPLICANT: Moyer, Richard W.
/ APPLICANT: Hall, Richard L.
/ APPLICANT: Gruidl, Michael E.
/ TITLE OF INVENTION: No. 5721352el Entomopoxvirus Expression System
/ NUMBER OF SEQUENCES: 40
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: David R. Saliwanchik
/ STREET: 2421 N.W. 41st Street, Suite A-1
/ CITY: Gainesville
/ STATE: Florida
/ COUNTRY: U.S.A.
/ ZIP: 32606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/107,755A
/ FILING DATE: 19-AUG-1993
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/827,658
/ FILING DATE: 30-JAN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/657,584
/ FILING DATE: 19-FEB-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Saliwanchik, David R.
/ REGISTRATION NUMBER: 31,794
```

```
/ REFERENCE/DOCKET NUMBER: UP114.C2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (904) 375-8100
/ TELEFAX: (904) 372-5800
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 6768 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: unknown
/ MOLECULE TYPE: DNA (genomic)
/ ORIGINAL SOURCE:
/ ORGANISM: Amsacta moorei entomopoxvirus
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: complement (65..1459)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1474..2151
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: complement (2239..2475)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 2502..2987
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 3080..6091
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: complement (6277..6768)
US-08-107-755A-1

Query Match      3.4%; Score 43; DB 1; Length 6768;
Best Local Similarity 47.8%; Pred. No. 0.11;
Matches 187; Conservative 0; Mismatches 200; Indels 4; Gaps 2;

QY 145 AACCATCAGCAGCTGCTGATGTTAACTGATCAATATCTGCTTAATACGACA 204
DB 2315 AACCATCTACTGTAGATGTTGGGAGATAAAGCTTGAAGATTAATTAACCTAAA 2256
QY 205 CCAACTGATTAATATCTTTCGACACATGTTATATCTATGTTGACTTTAATCAAT 264
DB 2255 GCAAAAAAATAAATAAGCTGTAATAATGATATTAATAATTAACATATATAT 2196
QY 265 AAATCAAGATATTAAGTGAAGTGTAGTATAGATTAAGTGAATGACATGA 324
DB 2195 TTATTCATTTTATTAATAAATAATGTTAGTATTAATTAATTAATTAATTAAT 2136
QY 325 GCTAATAGTTAGTACCTAAATTAAGTTGAGACATTCAAACCCATCAATTAAGTT 384
DB 2135 AAAAGTGTCCAGCTGATATTAATAAATGATATTAAGATTAATTAATTAATTAAT 2076
QY 385 ATTT--TTAGTAATTAAGTATTAAGTATTAATTAATTAATTAATTAATTAAT 442
DB 2075 CTCACATTAAGTATTAATTAAGCAAAATTAATTAATTAATTAATTAATTAATTAAT 2016
QY 443 GCAATTTTTCGCACTAATTAATTAAGTATTAATTAATTAATTAATTAATTAATTAAT 502
DB 2015 ACCGGTATTTCTCCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1958
QY 503 GTGATGCTCTTCTAAGATCTTAACCGTATG 533
DB 1957 GTGATACATATCTAATCAATCAATCAATTTTG 1927

RESULT 9
US-07-991-867B-1/c
/ Sequence 1, Application US/07991867B
/ Patent No. 5476781
/ GENERAL INFORMATION:
/ APPLICANT: Moyer, Richard W.
/ APPLICANT: Hall, Richard L.
```

APPLICANT: Gruidi, Michael E.
TITLE OF INVENTION: No. 5476781e1 Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/991,867B
FILING DATE: 12-DEC-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,685
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UFI14.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8457 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Amsacta moorei entomopoxvirus
FEATURE:
NAME/KEY: CDS
LOCATION: complement (65..1459)
FEATURE:
NAME/KEY: CDS
LOCATION: 1474..2151
FEATURE:
NAME/KEY: CDS
LOCATION: complement (2239..2475)
FEATURE:
NAME/KEY: CDS
LOCATION: 2502..2987
FEATURE:
NAME/KEY: CDS
LOCATION: 3080..6091
FEATURE:
NAME/KEY: CDS
LOCATION: complement (6277..6768)
US-07-991-867B-1
Query Match 3.4%; Score 43; DB 1; Length 8457;
Best Local Similarity 47.8%; Pred. No. 0.12;
Matches 187; Conservative 0; Mismatches 200; Indels 4; Gaps 2;
QY 145 AACATCAGCAGTGGTGTAGCTTAAGTGAATATCTTGTCTTTAACTACTAGA 204
DB 2315 AACCATCTACTAGTGTGGGAGATAAACGTTAGAGATAAAATTAATACCTAAA 2256
QY 205 CCAACTGATTAATCTTTCGAACACATCTTATCTATCTTGTGACTTAATCAATACT 264

DB 2255 GCAAAAAAAAAAATBAAGCTGTAAATGATATTAATAATTTGACATAACCAATATATTT 2196
QY 265 AATCCAGATATTTAGTAGAGTGTAGTATGATTAGAGTATGTTTAAAGCACTA 324
DB 2195 TTATTCATTTTATTAATAAATATTTAGTATTAATTAATTAATTAATTAATTA 2136
QY 325 GCTAATAGTATAGCTAATAATTTAGTTGGAGACATTCACCAACCCATCAATTAATAGTT 384
DB 2135 AAAAGTCTTCTAGCTGTATTTTAAATGAATATTAGAGTATATTTATCTAATAT 2076
QY 385 ATTT--TTAGTAATTTAGTTAATAGTATGTTATTTAATTAAGCTTTTAACTA 442
DB 2075 CTCACATTAGTATTAATAGCAAAATTTATATATTAATTAATAGATATATTAATTT 2016
QY 443 GCAATTTTTCAGCACTAATTAATGTTTGTGATTCAAATACCCCTAAGCCGTTAA 502
DB 2015 ACGGATATTCCTCTAATATTACATA--TTTATTAATCTAGATTTCAATAAATTCATAT 1958
QY 503 GTGATGCTCTTCTAGAAATCTTAACCGTATG 533
DB 1957 GTGATCTAATATCTAATACATCATATTTTG 1927
RESULT 10
US-08-544-332-1/C
Sequence 1, Application US/08544332
Patent No. 5935777
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidi, Michael E.
TITLE OF INVENTION: No. 5935777e1 Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gerard H. Bencen
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/544,332
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,867
FILING DATE: 07-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/107,755
FILING DATE: 19-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,685
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bencen, Gerard H.
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: UFI14.C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 1:

```
SEQUENCE CHARACTERISTICS:
LENGTH: 8457 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Amsacta moorei entomopoxvirus
FEATURE:
NAME/KEY: CDS
LOCATION: complement (65..1459)
FEATURE:
NAME/KEY: CDS
LOCATION: 1474..2151
FEATURE:
NAME/KEY: CDS
LOCATION: complement (2239..2475)
FEATURE:
NAME/KEY: CDS
LOCATION: 2502..2987
FEATURE:
NAME/KEY: CDS
LOCATION: 3080..6091
FEATURE:
NAME/KEY: CDS
LOCATION: complement (6277..6768)
US-08-544-332-1

Query Match      3.4%; Score 43; DB 2; Length 8457;
Best Local Similarity 47.8%; Pred. No. 0.12;
Matches 187; Conservative 0; Mismatches 200; Indels 4; Gaps 2;

OY 145 AACCATCAGCAGTGGTTGATAGTTAACTGATTAATCTGCTTTAACTAGCA 204
DB 2315 AACCATCTACTGTAGATGTTGGGAGATTAACGTTAGAGTAAATTAACCTAAA 2256
OY 205 CCACTGATTAATATCTTTCGAACACATGTATATCTATGTTGACTTTAATCAAT 264
DB 2255 GCAAAAAAATAAATGAAGCTGTAAATGATATTAATTAACATTAATATAT 2196
OY 265 AATCCAAATATTGTAGAGATGTAGATATAGATTAAGTGAAGTGAACACTAGA 324
DB 2195 TTATTCATTTTAAATTAATTAATGATGATTAATTAATTAATTAATTAAT 2136
OY 325 GCTAATAGTATAGTAAATTAAGTGAACATTAACACCCATCAATTAATAGT 384
DB 2135 AAAAGTCTCCACGTGATATTTAAATGATATAGATTAATTAATTAAT 2076
OY 385 ATTT--TTAGTAATTAAGTAAATAGTATAGTATTAATTAAGCTTTTACTA 442
DB 2075 CTCACATTAAGTAAATAGCAAAATTAATTAATTAATTAATTAATTAAT 2016
OY 443 GCAATTTTACCACTAACATTAAGTATAGTATTAATTAATTAATTAATTAAT 502
DB 2015 ACGGGATTTCTCCATTAATTAATTAATTAATTAATTAATTAATTAAT 1958
OY 503 GTGATGCTTTCTAGCAATCTTAACCGTATG 533
DB 1957 GTGATGCTATATCTAATCAATCACTATTTG 1927

RESULT 11
US-09-370-861A-1/c
Sequence 1, Application US/09370861A
Patent No. 6410221
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 6410221el Entomopoxvirus Expression System
FILE REFERENCE: UFI14.C4.D1
CURRENT APPLICATION NUMBER: US/09/370,861A
CURRENT FILING DATE: 1999-08-09
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PRIOR APPLICATION NUMBER: US 07/991,867
PRIOR FILING DATE: 1992-12-07
PRIOR APPLICATION NUMBER: US 08/107,755
PRIOR FILING DATE: 1993-08-19
PRIOR APPLICATION NUMBER: WO 92/14818
PRIOR FILING DATE: 1992-02-12
PRIOR APPLICATION NUMBER: US 07/827,685
PRIOR FILING DATE: 1992-01-30
PRIOR APPLICATION NUMBER: US 07/657,584
PRIOR FILING DATE: 1991-02-19
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 8457
TYPE: DNA
ORGANISM: Amsacta moorei entomopoxvirus
US-09-370-861A-1

Query Match      3.4%; Score 43; DB 4; Length 8457;
Best Local Similarity 47.8%; Pred. No. 0.12;
Matches 187; Conservative 0; Mismatches 200; Indels 4; Gaps 2;

OY 145 AACCATCAGCAGTGGTTGATAGTTAACTGATTAATCTGCTTTAACTAGCA 204
DB 2315 AACCATCTACTGTAGATGTTGGGAGATTAACGTTAGAGTAAATTAACCTAAA 2256
OY 205 CCACTGATTAATATCTTTCGAACACATGTATATCTATGTTGACTTTAATCAAT 264
DB 2255 GCAAAAAAATAAATGAAGCTGTAAATGATATTAATTAATTAATTAATAT 2196
OY 265 AATCCAAATATTGTAGAGATGTAGATATAGATTAAGTGAAGTGAACACTAGA 324
DB 2195 TTATTCATTTTAAATTAATTAATGATGATTAATTAATTAATTAATTAAT 2136
OY 325 GCTAATAGTATAGTAAATTAAGTGAACATTAACACCCATCAATTAATAGT 384
DB 2135 AAAAGTCTCCACGTGATATTTAAATGATATTAAGATTAATTAATTAAT 2076
OY 385 ATTT--TTAGTAATTAAGTAAATAGTATAGTATTAATTAAGCTTTTACTA 442
DB 2075 CTCACATTAAGTAAATAGCAAAATTAATTAATTAATTAATTAATTAAT 2016
OY 443 GCAATTTTACCACTAACATTAAGTATAGTATTAATTAATTAATTAATTAAT 502
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OY 503 GTGATGCTTTCTAGCAATCTTAACCGTATG 533
DB 1957 GTGATGCTATATCTAATCAATCACTATTTG 1927

RESULT 12
US-08-916-421B-1/c
Sequence 1, Application US/08916421B
Patent No. 6503729
GENERAL INFORMATION:
APPLICANT: Built et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococc
Patent No. 6503729
FILE REFERENCE: PB275
CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1664976
TYPE: DNA
ORGANISM: Methanococcus jannaschii
FEATURE:
NAME/KEY: misc_feature
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OTHER INFORMATION: n equals a, t, c, or g


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/ OTHER INFORMATION: /product= "E3 exon"
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: 1290..1559
/ OTHER INFORMATION: /product= "E5 exon"
US-08-119-512-1

Query Match      3.4%; Score 42; DB 1; Length 4539;
Best Local Similarity 47.5%; Pred. No. 0.17;
Matches 155; Conservative 0; Mismatches 170; Indels 1; Gaps 1;

QY 20 TATACATATCCATTTCACATAATGAAACCAATTAATTAATAAACTAAAAAACT 79
DB 1822 TATCAATATATATTATATATATATATATATATATATATATATATATATATAT 1881
QY 80 TTATCACCGTACAGAGAAAGAGACATCACTGCTATTAGTTTATGCAATTAACACC 139
DB 1882 TGTATTGGAAATGAGCATACGATTAATCATATATACCATAGTAAATTAATTTGAGAGCTA 1941
QY 140 CTTGCAACCATCAGACAGTGTGATAGTATTAAGTATCTATATCTGCTTTAATAC 199
DB 1942 AGTTAGATATTTACGATTTATGATATAACAGATTAACCTTAATATATATTTAA 2001
QY 200 TAGCACCACTGATATAATCTTTCCAGACATGTTATATCTATGTTGACTTTAATCA 259
DB 2002 TATATAAAAAATATATATAT -ACCATATATATATATATATATATATATATATTA 2060
QY 260 ATACTTAATCCAGATATATTAGTAGAGATGTATAGTATTAAGTGATGTTGAATGCA 319
DB 2061 ATTAATAATTAATATATATATATATATATATATATATATATATATATATATATAGAA 2120
QY 320 CTAGAGCTAATAGTAGTAA 345
DB 2121 ATTTCTTATATTTAGAGGGTAA 2146

RESULT 15
US-08-488-015B-1
/ Sequence 1, Application US/08488015B
/ Patent No. 5780272
/ GENERAL INFORMATION:
/ APPLICANT: Jarell, Kevin A.
/ TITLE OF INVENTION: INTRON-MEDIATED RECOMBINANT TECHNIQUES
/ TITLE OF INVENTION: AND REAGENTS
/ NUMBER OF SEQUENCES: 29
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Foley, Hoag & Eliot
/ STREET: One Post Office Square
/ CITY: Boston
/ STATE: MA
/ COUNTRY: USA
/ ZIP: 02109
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: ASCII (text)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/488,015B
/ FILING DATE: 07-JUN-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Vincent, Matthew P.
/ REGISTRATION NUMBER: 36,709
/ REFERENCE/DOCKET NUMBER: HUV-008.02
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 832-1000
/ TELEFAX: (617) 832-7000
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: both
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/ MOLECULE TYPE: other nucleic acid
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: 969..1259
/ OTHER INFORMATION: /product= "E3 exon"
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: 1290..1559
/ OTHER INFORMATION: /product= "E5 exon"
US-08-488-015B-1

Query Match      3.4%; Score 42; DB 1; Length 4539;
Best Local Similarity 47.5%; Pred. No. 0.17;
Matches 155; Conservative 0; Mismatches 170; Indels 1; Gaps 1;

QY 20 TTATCAATATCCATTTCACATAATGAAACCAATTAATTAATAAACTAAAAAACT 79
DB 1822 TATCAATATATATTATATATATATATATATATATATATATATATATATATAT 1881
QY 80 TTATCACCGTACAGAGAAAGAGACATCACTGCTATTAGTTTATGCAATTAACACC 139
DB 1882 TGTATTGGAAATGAGCATACGATTAATCATATATACCATAGTAAATTAATTTGAGAGCTA 1941
QY 140 CTTGCAACCATCAGACAGTGTGATAGTATTAAGTATCTATATCTGCTTTAATAC 199
DB 1942 AGTTAGATATTTACGATTTATGATATAACAGATTAACCTTAATATATATTTAA 2001
QY 200 TAGCACCACTGATATAATCTTTCCAGACATGTTATATCTATGTTGACTTTAATCA 259
DB 2002 TATATAAAAAATATATATAT -ACCATATATATATATATATATATATATATATTA 2060
QY 260 ATACTTAATCCAGATATATTAGTAGAGATGTATAGTATTAAGTGATGTTGAATGCA 319
DB 2061 ATTAATAATTAATATATATATATATATATATATATATATATATATATATATATAGAA 2120
QY 320 CTAGAGCTAATAGTAGTAA 345
DB 2121 ATTTCTTATATTTAGAGGGTAA 2146
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Search completed: July 17, 2004, 14:15:58
Job time : 91 secs

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Query Match 381: 5.5%; Score 69; DB 13; Length 1125;
Best Local Similarity 70.8%; Pred. No. 6e-06;
Matches 138; Conservative 0; Mismatches 45; Indels 12; Gaps 3;

QY 300 TAAGTGATGTTTGAATGCACTAGAGCTAAATAGTTAGTAAATAGTTGGAGACAT 359
DB 928 TAAGGAAATGTTGAATACACTAGAACTAAATAGTTAGCTGCTAAATTT-----GAGACAT 874
QY 360 TCAAAACCCCTATCAATATATAGTATTTTATAGTAAATAGTAAATAGTACTTGTAT 419
DB 873 CTAAACAGCTTAGCTAAATATTTTACCTATCAACTACTTT-----TAGCAAAATAGGTAA 820
QY 420 TTATAGCTAGCTTTTCTTACTAGCAATTTTTCACCACTAACAATAGTTTATGTGTA 479
DB 819 TAGTTAGCTAGCTAATTCACCTAAC-AATTTTTCAGCTAAGTAACTATTTATCTCTAGTGA 761
QY 480 TTCAAAATACCCCTAA 494
DB 760 TTCAAAACACTCCTAA 746

RESULT 7
US-10-425-114-20790/c
; Sequence 20790, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 20790
; LENGTH: 2646
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LTB3245-244-G2_FLI
US-10-425-114-20790

Query Match 382: 5.5%; Score 69; DB 13; Length 2646;
Best Local Similarity 70.8%; Pred. No. 9.6e-06;
Matches 138; Conservative 0; Mismatches 45; Indels 12; Gaps 3;

QY 300 TAAGTGATGTTTGAATGCACTAGAGCTAAATAGTTAGTAAATAGTTGGAGACAT 359
DB 2541 TAAGGAAATGTTGAATACACTAGAACTAAATAGTTAGCTGCTAAATTT-----GAGACAT 2487
QY 360 TCAAAACCCCTATCAATATATAGTATTTTATAGTAAATAGTAAATAGTACTTGTAT 419
DB 2486 CTAAACAGCTTAGCTAAATATTTTACCTATCAACTACTTT-----TAGCAATTAGGTAA 2433
QY 420 TTATAGCTAGCTTTTCTTACTAGCAATTTTTCACCACTAACAATAGTTTATGTGTA 479
DB 2432 TAGTTAGCTAGCTAATTCACCTAAC-AATTTTTCAGCTAAGTAACTATTTATCTCTAGTGA 2374
QY 480 TTCAAAATACCCCTAA 494
DB 2373 TTCAAAACACTCCTAA 2359

RESULT 8
US-10-425-114-17711/c
; Sequence 17711, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:

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QY 427 CTAGCTTTTCTTCTAGCAATTTTCTAGCCACTACATTTAGTTTACTGTA 479
Db 1891 TATATTTTCTTATTAATAATTTTCTATATATTTTCTATTTTCTATTTTAA 1933

RESULT 12
US-10-425-114-13740/c
; Sequence 13740, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425.114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO: 13740
; LENGTH: 1144
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB143-037-C9_FLI
US-10-425-114-13740

Query Match 4.5%; Score 56.6; DB 13; Length 1144;
Best Local Similarity 62.2%; Pred. No. 0.0054;
Matches 125; Conservative 0; Mismatches 69; Indels 7; Gaps 2;

QY 291 AGTATGATTTAGTGATGATTTTGAATGCACTAGACTAATAGTTAGTCTAAATAGT 350
Db 397 AGGATGTACTAAGGGGGGTTTGAAGGCACTAGACTAATAGTTAGTGAACAAAAAT 338
QY 351 TGGAGACATTCGAACACCCCTATCATTTATTTAGTTATTTTGTAAATAGTATAGTTA 410
Db 337 ACTAG---TGAATTAGCTTACGACTATTTGCTAATTTGCTAAAGTAGCTAATAGCTG 282
QY 411 GTTATGATTTATTAAGCTAGCTTTTCTTCTAGCAATTTTCTAGCCAACTAACAACTAGT 470
Db 281 AACTATTAGCTAGACTGTTTGAAGTCTTCAAGCTAATTTT---ACGGCTAATCTATTAGC 225
QY 471 TTTAGTGTATTCGAATACCCC 491
Db 224 TTTAGCGATTCGAACACACAC 204

RESULT 13
US-10-239-676-14/c
; Sequence 14, Application US/10239676
; Publication No. US20030082609A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
; FILE REFERENCE: 5013.1003
; CURRENT APPLICATION NUMBER: US/10/239.676
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: PCT/EP01/03968
; DE 10019058.8
; DE 10019173.8
; DE 10032529.7
; DE 10043826.1
; PRIOR FILING DATE: 2001-04-06
; 2000-04-06
; 2000-04-07
; 2000-06-30
; 2000-09-01

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NUMBER OF SEQ ID NOS: 228
SEQ ID NO 14
LENGTH: 10286
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-239-676-14

Query Match 4.5%; Score 56; DB 15; Length 10286;
Best Local Similarity 45.0%; Pred. No. 0.025; Mismatches 255; Indels 0; Gaps 0;
Matches 209; Conservative 0;

QY 25 AATATCCATTTCACCTAATAGAAAACCAATTATTTAAAAAACCCTTAATC 84
DB 3104 AATTTAAATATTCATTAATCTTAAAAACAAAAATTAAAAAACAACCTAAACCAAAAAC 3045
QY 85 ACCGTACGAGAGAGAGACATCACTGCTATTAGTTTATGCACTTTAAACACCCCTTCG 144
DB 3044 CAATATCCCTTAAAAAATAATTAATACCTAAAAATATTGCTAAATAATTAAAAAATA 2985
QY 145 AACCATCAGCAGTGGTGTAGTGTACTGATCTAATATCTGTCTTTAATCTAGCA 204
DB 2984 AAAAAATTAATTAATTTTATTTTATTTTATTTAATTAATTAATCAATCCAAAAA 2925
QY 205 CCACTGATATATATCTTTCGACACATGTTATTAATCTATGTTGACTTTAATCAATCT 264
DB 2924 CTAAACAAATTTAAACCAAAAAACATCTAATACATTTTAAATTAATTAACCTTCAT 2865
QY 265 AAATCCAGATATTTAGTAGAGATGTTAGTAGATTAGAGTATTTGAATGACCTAGA 324
DB 2864 TAAAAAAATCGATTAATTAATTTATTTATTAATTAATTAATTAATTAATTAATTA 2805
QY 325 GCTAATAGTATAGTAAATTAATTTAGTAGAGATTCACCAACCCATCAATTAATAGT 384
DB 2804 TCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTTCCCAAT 2745
QY 385 ATTTTATAGTAATTTAGTAAATTTAGTAAATTTAGTAAATTTAGTAAATTTAGTAA 444
DB 2744 AAAACCTTAAAAAAATTTAATTTTATTTAGTAAATTTAGTAAATTTAGTAAATTA 2685
QY 445 AATTTTGGCACTAACATTAATTTAGTAAATTTAGTAAATTTAGTAAATTTAGTAA 488
DB 2684 ACTAAGTAATTAATTAATTTAGTAAATTTAGTAAATTTAGTAAATTTAGTAAAC 2641

RESULT 14
US-10-240-453-22/C
Sequence 22, Application US/10240453
Publication No. US20030148326A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA
TITLE OF INVENTION: Transcription
TITLE OF INVENTION: By Means of Assessing the Methylation Status of Genes Associated
FILE REFERENCE: 5013.1009
CURRENT APPLICATION NUMBER: US/10/240,453
CURRENT FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: PCT/EP01/03973
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 350
SEQ ID NO 22

LENGTH: 10286
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-453-22

Query Match 4.5%; Score 56; DB 15; Length 10286;
Best Local Similarity 45.0%; Pred. No. 0.025; Mismatches 255; Indels 0; Gaps 0;
Matches 209; Conservative 0;

QY 25 AATATCCATTTCACCTAATAGAAAACCAATTATTTAAAAAACCCTTAATC 84
DB 3104 AATTTAAATATTCATTAATCTTAAAAACAAAAATTAAAAAACAACCTAAACCAAAAAC 3045
QY 85 ACCGTACGAGAGAGAGACATCACTGCTATTAGTTTATGCACTTTAAACACCCCTTCG 144
DB 3044 CAATATCCCTTAAAAAATAATTAATACCTAAAAATATTGCTAAATAATTAAAAAATA 2985
QY 145 AACCATCAGCAGTGGTGTAGTGTACTGATCTAATATCTGTCTTTAATCTAGCA 204
DB 2984 AAAAAATTAATTAATTTTATTTTATTTTATTTAATTAATTAATTAATCAATCCAAAAA 2925
QY 205 CCACTGATATATCTTTCGACACATGTTATTAATCTATGTTGACTTTAATCAATCT 264
DB 2924 CTAAACAAATTTAAACCAAAAAACATCTAATACATTTTAAATTAATTAACCTTCAT 2865
QY 265 AAATCCAGATATTTAGTAGAGATGTTAGTAGATTAGAGTATTTGAATGACCTAGA 324
DB 2864 TAAAAAAATCGATTAATTAATTTATTTAATTAATTAATTAATTAATTAATTAATTA 2805
QY 325 GCTAATAGTATAGTAAATTTAGTAAATTTAGTAAATTTAGTAAATTTAGTAAATTTAGT 384
DB 2804 TCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTTCCCAAT 2745
QY 385 ATTTTATAGTAATTTAGTAAATTTAGTAAATTTAGTAAATTTAGTAAATTTAGTAA 444
DB 2744 AAAACCTTAAAAAAATTTAATTTTATTTAGTAAATTTAGTAAATTTAGTAAATTA 2685
QY 445 AATTTTGGCACTAACATTAATTTAGTAAATTTAGTAAATTTAGTAAATTTAGTAA 488
DB 2684 ACTAAGTAATTAATTAATTTAGTAAATTTAGTAAATTTAGTAAATTTAGTAAAC 2641

RESULT 15
US-10-240-454-19
Sequence 19, Application US/10240454
Publication No. US20040067491A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with Metabolism
FILE REFERENCE: 5013.1010
CURRENT APPLICATION NUMBER: US/10/240,454
CURRENT FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: PCT/EP01/04016
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 68
SEQ ID NO 19
LENGTH: 6219
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)

US-10-240-454-19

Query Match 4.4%; Score 55.2; DB 13; Length 6219;

Best Local Similarity 51.0%; Pred. No. 0.029;

Matches 155; Conservative 0; Mismatches 148; Indels 1; Gaps 1;

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DB 2150 TTAGATTTTGTATTTGGTTGGTTGCTTTTATATTTAATAGTTTTTTGAAGTTT 2209
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 210 TCATATATCTTTCACACATGTTATTCATTTGTTGACTTATCATCATCTAAATC 269
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2210 TTATATATTTTATATTAAGTTAAGTTAAGTTAATATTAAGTAAGTATTAATTT 2269
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 270 CAAGATATTAGTAGAGATGTTAGTATAGATTAAAGTGATGTTGAATGCACTAGAGCTAA 329
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2270 AAAAAATTAATGAAGATTAAGTTATTTTGAAGAAAGTTTATGAGGTTGAA 2329
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 330 TAGTATAGCTAAATAGTTGAGACATTCAAACCCATCAATTATTAAGTTATTTT 389
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2330 TTTATTTTGGTATTAAGTGGGTTTGTGTAAGAAATTGA-AATTATTTATTAATTT 2388
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 390 TAGTAATTAAGTTAATAGTTAGTTAGTTATTTAATAAGCTAGCTTTTACTAGCAATTT 449
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2389 GGGGAAATTTGAATTGTAGTTAGTTAGTTTTTAGGGTTTATATGTAAGAAAGTTA 2448
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 450 TTTA 453
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2449 TTTA 2452
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Search completed: July 17, 2004, 14:23:51
Job time : 458 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 17, 2004, 12:17:49 ; Search time 2465 Seconds
(without alignments)
15106.750 Million cell updates/sec

Title: US-09-718-754A-1
Perfect score: 1247
Sequence: 1 atccgacataaagtcgtgatt.....agagtcgctgacactagca 1247

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: em_escba:*
2: em_escbm:*
3: em_escbn:*
4: em_escbu:*
5: em_escbv:*
6: em_escpl:*
7: em_escro:*
8: em_escr:*
9: gb_esc1:*
10: gb_esc2:*
11: gb_esc3:*
12: gb_esc4:*
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14: gb_esc6:*
15: em_escfun:*
16: em_escfm:*
17: em_escgm:*
18: em_escinv:*
19: em_escpin:*
20: em_escvrt:*
21: em_escfun:*
22: em_escmam:*
23: em_escmus:*
24: em_escpro:*
25: em_escrod:*
26: em_escphg:*
27: em_escvrt1:*
28: gb_gss2:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	665.2	53.3	877	28	BZ791704 PUGBR37TD
2	614.2	49.3	933	28	BZ791700 PUGBR37TB
3	590.2	47.3	912	29	CG178223 PUFOS05TD
4	399	32.0	871	29	CG176077 PUBBP90TD

C 5	290	23.3	849	29	CG178220	CG178220 PUFOS05TB
6	251.4	20.2	647	29	CG678977	CG678977 OGJAI29TV
7	201.8	16.2	860	29	CG155338	CG155338 PUH1826TB
8	193	15.5	861	29	CG037363	CG037363 PUFML59TD
9	191.4	15.3	872	29	CG098858	CG098858 PUF2Q26TD
10	191.4	15.3	884	29	CG455835	CG455835 PU1K070TD
11	191.4	15.3	891	28	BZ795791	BZ795791 PUFQM22TB
12	191.4	15.3	889	28	BZ795799	BZ795799 PUFQM22TB
13	190.6	15.3	856	28	BZ786431	BZ786431 PUGBR29TB
14	187.4	15.0	844	28	CG014365	CG014365 PUBRV07TD
15	187.4	15.0	905	29	CG132370	CG132370 PUGH42TB
16	185	14.8	791	28	CC013848	CC013848 PUGH94TD
17	173.8	13.9	852	28	CC007983	CC007983 PUDFV11TD
18	166.6	13.4	805	28	BZ825667	BZ825667 PUGFP95TB
19	157	12.6	696	29	CG043582	CG043582 PUFAR11TD
20	156.4	12.5	756	29	CG236449	CG236449 OGZAA02TH
21	155.6	12.5	933	29	CG330662	CG330662 OG3CN08TV
22	151	12.1	692	28	BZ547228	BZ547228 OGALM25TC
23	151	12.1	836	29	CG098889	CG098889 PUFEX22TB
24	147.2	11.8	730	29	CG005872	CG005872 ZUAF457TV
25	147.2	11.8	803	29	CG277254	CG277254 OGXF15TV
26	146.2	11.7	666	29	CG853480	CG853480 ZMHB035
27	145.8	11.7	770	28	CG379956	CG379956 PUFBO21TD
28	145.8	11.7	975	29	CG070123	CG070123 PUFPO06TD
29	143.8	11.5	811	28	CG373252	CG373252 PUFJC47TD
30	143.2	11.5	871	28	BZ679873	BZ679873 PUFBS93TD
31	141.8	11.4	708	28	BZ525504	BZ525504 OGAGA93TC
32	141.8	11.4	786	28	CC017207	CC017207 PUFCD87TD
33	136.6	11.0	913	28	CG379954	CG379954 PUFBO21TD
34	134.2	10.8	620	28	BZ622271	BZ622271 1977d04.9
35	133.8	10.7	714	28	BZ802691	BZ802691 PUFBE30TB
36	133.8	10.7	770	28	BZ535488	BZ535488 OGAGH65TC
37	133.2	10.7	313	28	BZ686702	BZ686702 PUBJ785TD
38	133.2	10.7	815	28	BZ703676	BZ703676 PUFCC32TD
39	133.2	10.7	867	29	CG168508	CG168508 PUFPI42TB
40	133.2	10.7	917	29	CG441781	CG441781 OGVM787TV
41	133	10.7	440	29	CG642979	CG642979 OGUCN86TV
42	133	10.7	862	29	CG157331	CG157331 PUFYH44TD
43	132.6	10.6	862	28	CC014963	CC014963 PUDAI18TD
44	132.2	10.6	755	28	BZ541495	BZ541495 OGAGB11TC
45	131.4	10.5	263	29	CG034521	CG034521 PUFSP95TD

ALIGNMENTS

RESULT 1
LOCUS BZ791704 877 bp DNA linear GSS 17-MAR-2003
DEFINITION PUGBR37TD ZM.0.6.1.0_KB Zea mays genomic clone ZMMBTa331H02,
genomic survey sequence.
ACCESSION BZ791704
VERSION BZ791704.1 GI:28988373
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 877)
AUTHORS Whitehead, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J., and
Bennetzen, J.
TITLE Maize Genomics Consortium
JOURNAL Unpublished (2003)
COMMENT Other GSSs: PUGBR37TB
Contact: Cathy Whitehead
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitehead@cigr.org
Seq primer: TP

FEATURES
source
Class: sheared ends.
Location/Qualifiers
1. 877
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMBR331H02"
/clone_lib="ZM 0.6 1.0 KB"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
cot selected genomic DNA library"

ORIGIN

Query Match 53.3%; Score 665.2; DB 28; Length 877;
Best Local Similarity 99.6%; Pred. No. 1.5e-127;
Matches 667; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 578 TGAATTAATTAATTTTCAATGCGGTTCTTAAAGCAAAACCGCAAGCTATGATATTAC 637
DB 8 TGATATATATATTTTCAATGCGGTTCTTAAAGCAAAACCGCAAGCTATGATATTAC 67
QY 638 ACTAGCGGCTGCTAAGAAACCGCGTGTAAAGATTTTACCTAGCGGTTGTGA 697
DB 68 ACTAGCGGCTGCTAAGAAACCGCGAGTCTAAAGATTTTACCTAGCGGTTGTGA 127
QY 698 ACAACTGCTGTGAAGAAACCGGATTCCTAAGCCCTAGCTTGCATGCGACATAA 757
DB 128 ACAAGCTGCTGGAAGAAACCGGATTTCTAAGCCCTAGCTAGACATGCGACATAA 187
QY 758 AAACGTCACTGAATATAGCTTCAAGATGCTCACTATAGAGCTTCTATGATTTAGTGT 817
DB 188 AAACGTCACTGAATATAGCTTCAAGATGCTCACTATAGAGCTTCTATGATTTAGTGT 247
QY 818 AGAAGCTATGATGATGACCAAGTCCGATTTTAAACCAATTAATTAATTAATTAAT 877
DB 248 AGAAGCTATGATGATGACCAAGTCCGATTTTAAACCAATTAATTAATTAATTAAT 307
QY 878 AATATATATAGTGTCTGAATTCGATTTCTATAGTAATGTTGCTTGCAGCCGCAAT 937
DB 308 AATATATATAGTGTCTGAATTCGATTTCTATAGTAATGTTGCTTGCAGCCGCAAT 367
QY 938 AAGATTAACATTCGTGCTCAAGAAATCCACATTAATCAAGGTCATGCGCGCGCA 997
DB 368 AAGATTAACATTCGTGCTCAAGAAATCCACATTAATCAAGGTCATGCGCGCGCA 427
QY 998 CGTACCCATCCACGCGTGTGCGGAGGACACGTTGGCTGACCGGCAATTTGCCGA 1057
DB 428 CGTACCCATCCACGCGTGTGCGGAGGACACGTTGGCTGACCGGCAATTTGCCGA 487
QY 1058 TCAGACAGTGAACAGACCGGACCAATAGAAAGAAAGACAGACGCGCGCGCACCGCG 1117
DB 488 TCAGACAGTGAACAGACCGGACCAATAGAAAGAAAGACAGACGCGCGCGCACCGCG 547
QY 1118 AGTAGGTGATGATCAACGCTAGCTGTATTTTGGAGAGCGTGTCTGTAAATACGTA 1177
DB 548 AGTAGGTGATGATGATCAACGCTAGCTGTATTTTGGAGAGCGTGTCTGTAAATACGTA 607
QY 1178 CCTTTCACAAAGCGAGGCGAGGAGAGAGATATGCTAGCTAGACAGAGAGATGCGTA 1237
DB 608 CCTTTCACAAAGCGAGGCGAGGAGAGAGATATGCTAGCTAGACAGAGATGCGTA 667
QY 1238 GCAACTAGCA 1247
DB 668 GCAACTAGCA 677

RESULT 2
BZ791700/c 933 bp DNA linear GSS 17-MAR-2003
LOCUS BZ791700
DEFINITION PUGBR37TB_ZM_0.6_1.0_KB_Zea_mays_genomic_clone_ZMBR331H02,
genomic survey sequence.
ACCESSION BZ791700
VERSION BZ791700.1 GI:28988365

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
GSS.
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 933)
Whiteley,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,D. and
Benner,J.
Maize Genomics Consortium
Unpublished (2003)
Other_GSSs: PUGBR37TD
Contact: Cathy Whiteley
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whiteley@cigr.org
Seq primer: TR
Class: sheared ends.

FEATURES

source

Location/Qualifiers
1. 933
/organism="Zea mays"
/mol_type="genomic DNA"
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cot selected genomic DNA library"

ORIGIN

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Best Local Similarity 99.5%; Pred. No. 5.5e-117;
Matches 616; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 629 GATATTTACATGAGGCGCTCTAAGAAACCGCGCTGTAAAGATTTTACACTAGC 688
DB 933 GATATTTACATGAGGCGCTCTAAGAAACCGCGAGTGTAAAGATTTTACACTAGC 874
QY 689 GGTGTGAACAACCTGCTGTGAAGAAACCGGATTCCTAAGCCCTAGCTTGCATCG 748
DB 873 GGTGTGAACAACCTGCTGTGAAGAAACCGGATTCCTAAGCCCTAGCTTGCATCG 814
QY 749 CGACATTAAGAAACCTGCTGAATATAGCTAGATGCTCACTATAGGCTTCTATGAC 808
DB 813 CGACATTAAGAAACCTGCTGAATATAGCTAGATGCTCACTATAGGCTTCTATGAC 754
QY 809 TTATGTTTGAACATGATATTGTAGTCAACCAAGTCCGATTTTAAATTAACCAATACTA 868
DB 753 TTATGTTTGAACATGATATTGTAGTCAACCAAGTCCGATTTTAAATTAACCAATACTA 694
QY 869 AATACTAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 928
DB 693 AATACTAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 634
QY 929 GCGGCAATTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 988
DB 633 GCGGCAATTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 574
QY 989 GCGGCGGACGATCCATCCACGCGTGTGCGGAGGACACGTTGGCTGACCGGACA 1048
DB 573 GCGGCGGACGATCCATCCACGCGTGTGCGGAGGACACGTTGGCTGACCGGACA 514
QY 1049 GTTGCCGATGACAGTGAACAGCCGACCAATAGAAAGAAAGACAGACGCGCGCG 1108
DB 513 GTTGCCGATGACAGTGAACAGCCGACCAATAGAAAGAAAGACAGACGCGCGCG 454
QY 1109 GCACCGCGAGTAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1168
DB 453 GCACCGCGAGTAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 394

QY	1169	AATACGTAGCCCTTCACAAGGAGGACAAGGCGGAGAGATATGTCAGCTAGCAGACA	1228
Db	393	AATACGTAGCCCTTCACAAGGAGGACAAGGCGGAGAGATATGTCAGCTAGCAGACA	334
QY	1229	GAGTGCCTAGCAACTAGCA	1247
Db	333	GAGTGCCTAGCAACTAGCA	315
RESULT 3			
LOCUS	CG178223	912 bp	DNA linear GSS 21-AUG-2003
DEFINITION	PUFOS05TD ZM 0.6 1.0 KB Zea mays genomic clone ZMMBT0711B09,		
ACCESSION	CG178223		
VERSION	CG178223.1		
KEYWORDS	GSS.		
SOURCE	Zea mays		
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.		
REFERENCE	1 (bases 1 to 912)		
AUTHORS	Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Benick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,D. and Renneisen,J.		
TITLE	Maize Genomics Consortium		
JOURNAL	Unpublished (2003)		
COMMENT	Other_GSSs: PUFOS05TB		
	Contact: Cathy Whitelaw		
	TIGR		
	9712 Medical Center Drive, Rockville, MD 20850, USA		
	Tel: 301-838-5843		
	Fax: 301-838-0208		
	Email: whitelaw@cigr.org		
	Seq primer: TF		
	Class: sheared ends.		
FEATURES	Location/Qualifiers		
source	1..912		
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Best Local Similarity	99.5%;	Pred. No. 5.2e-112;	
Matches 592;	Conservative 0;	Mismatches 3;	Indels 0; Gaps 0;
QY	653	AAGAAACCGCCCGTCTAAAGATATTTACACTAGCGGTTGTGAAACAACCTGCTGTGA	712
Db	12	AAGAAACCGCCGAGCTCTAAAGATATTTACACTAGCGGTTGTGAAACAACCTGCTGTGA	71
QY	713	AAAAGCGGATTCCTACTAGACCCCTAGAGCTTGACATGCGGCACTPAAAAAACGTCAGTGA	772
Db	72	AAAAGCGGATTTCTACTAGACCCCTAGAGCTTGACATGCGGCACTPAAAAAACGTCAGTGA	131
QY	773	TAGCTTAGATCGTCACTATAGAGCTTCTATGTACTTAGTGTTAGAACTGATTTGTA	832
Db	132	TAGCTTAGATCGTCACTATAGAGCTTCTATGTACTTAGTGTTAGAACTGATTTGTA	191
QY	833	GTGCAACCAAGTCCGATTTTAATTAAACAATACTAAATCTAGTAATTAATCTAGTGG	892
Db	192	GTGCAACCAAGTCCGATTTTAATTAAACAATACTAAATTAATTAATTAATCTAGTGG	251
QY	893	TCTGAATTCGATTTCTATAGTAATGTTGCTTGCAAGCCGCAATATAGTAACATTCGT	952
Db	252	TCTGAATTCGATTTCTATAGTAATGTTGCTTGCAAGCCGCAATATAGTAACATTCGT	311

Oy	953	CGTCACAGAAATCCACATTTTCATCAATCAAGTCATAGCGCGCCGCCACAGTACCCATCCGACG	1012
Db	312	CGTCACAGAAATCCACATTTTCATCAATCAAGTCATAGCGCGCCGCCACAGTACCCATCCACG	371
Oy	1013	CGTCGCTGCGGAGGACAGCTGTTGGCTGACCGGACAGTTGGCCGATCAGACAGTGGACAG	1072
Db	372	CGTCGCTGCGGAGGACAGCTGTTGGCTGACCGGACAGTTGGCCGATCAGACAGTGGACAG	431
Oy	1073	ACCGGACAAATGAAAGAAAGACGACGCGCGCGCCACCCGCGATAGTGTGATGTC	1132
Db	432	ACCGGACAAATGAAAGAAAGACGACGCGCGCGCCACCCGCGATAGTGTGATGTC	491
Oy	1133	ACCGTAGCTGAGCTTTTGTGAGAGCGTCGTCGTAAATACGTAGCCCTTCCACAACGCA	1192
Db	492	ACCGTAGCTGAGCTTTTGTGAGAGCGTCGTCGTAAATACGTAGCCCTTCCACAACGCA	551
Oy	1193	GGCAAGGGGGGAGAGAGATCGTCAAGCTACAGAGAGAGTGCCTAGCACTAGCA	1247
Db	552	GGCAAGGGGGGAGAGAGATCGTCAAGCTACAGAGAGAGTGCCTAGCACTAGCA	606
RESULT 4			
LOCUS	CG176077	871 bp	linear
DEFINITION	PUBBP90TD ZM 0.6 1.0 KB Zea mays genomic clone ZMBBTA0631012,		
ACCESSION	CG176077		
VERSION	CG176077.1	GI:34066875	
KEYWORDS	GSS.		
SOURCE	Zea mays		
ORGANISM	Zea mays		
REFERENCE	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD clade; Panicoideae; Andropogoneae; Zea.		
AUTHORS	1 (bases 1 to 871) WhiteLaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T., Renwick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and Bennezen,J.		
TITLE	Maize Genomics Consortium		
JOURNAL	Unpublished (2003)		
COMMENT	Other_GSSs: PUBBP90TB Contact: Cathy WhiteLaw TIGR		
	9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843 Fax: 301-838-0208 Email: whiteLaw@cigr.org Seq primer: TF Class: sheared ends.		
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source	1..871		
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	/strain="B73"		
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	/clone_1lb="ZM 0.6 1.0 KB"		
	/note="Vector: pCR4-TObO; Site_1: EcoRI; 0.6-1.0 kb high Cot selected genomic DNA library"		
ORIGIN			
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Best local Similarity	100.0%; Pred. No. 2e-72;		
Matches 399; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Oy	849	TTTTAATTAAACCAATCTGTAATACTAGTAATTAATTAATCTAGTGTGATTCGATTCTTCT	908
Db	1	TTTTAATTAAACCAATCTGTAATACTAGTAATTAATTAATCTAGTGTGATTCGATTCTTCT	60
Oy	909	ATAGTAATGTTTGCTTGCAAGCCGCAAAATGAGTAACATTCGTCGACAGAAATCCAC	968
Db	61	ATAGTAATGTTTGCTTGCAAGCCGCAAAATGAGTAACATTCGTCGTCACAGAAATCCAC	120

QY 969 ATTACATCAAGGTCATGCGCGCGCCGACAGTACCCTCCAGCGCTCGCTCGGAGAC 1028
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Db 121 ATTACATCAAGGTCATGCGCGCGCCGACAGTACCCTCCAGCGCTCGCTCGGAGAC 180
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|
Db 181 ACGTGTGGCTTACCGGACAGTTGGCCGATCAGACAGTGGACAGACCGGACAATAGAGA 240
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QY 1089 AGAAGACGACGACGCGGGGGGACCGCCGAGTAGAGTGCATGCTCAGCTAGCTAGCTT 1148
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|
Db 241 AGAAGACGACGACGCGGGGGGACCGCCGAGTAGAGTGCATGCTCAGCTAGCTAGCTT 300
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QY 1149 TTTCGACAGCGTCTGTCTGTAATACCTAGCCCTTCACAAGCGAGGCAAGGGGGAGAGA 1208
|
|
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Db 301 TTTCGACAGCGTCTGTCTGTAATACCTAGCCCTTCACAAGCGAGGCAAGGGGGAGAGA 360
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QY 1209 GTATCTCAGCTTACGACAGAGAGTGGCTTGCACACTTGCA 1247
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Db 361 GTATCTCAGCTTACGACAGAGAGTGGCTTGCACACTTGCA 399
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RESULT 5

CG178220/c 849 bp DNA linear GSS 21-AUG-2003
LOCUS PUFQ505TB.ZM.0.6.1.0.KB.Zea.mays.genomic.clone.ZM5BTa0711B09,
DEFINITION genomic survey sequence.
ACCESSION CG178220
VERSION CG178220.1 GI:34069281
KEYWORDS GSS.

SOURCE

ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 849)
White, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J., and
Bennetzen, J.,
Maize Genomic Consortium
Unpublished (2003)
Other_GSSs: PUFQ505TB
Contact: Cathy Whitelaw

REFERENCE

AUTHORS Bennettzen, J.,
Maize Genomic Consortium
Unpublished (2003)
Other_GSSs: PUFQ505TB
Contact: Cathy Whitelaw

TITLE

JOURNAL

COMMENT

TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@cigr.org
Seq primer: TR
Clas: sheared ends.

FEATURES

source

1. 849
Location/Qualifiers
/organism="Zea mays"
/mol_type="genomic DNA"
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 7.4e-50;
Matches 290; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 958 CAGAAATCCATTCATCATCAAGTCCATGCGCGCGCCGACAGTACCCTCCAGCGGTCG 1017
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|
|
Db 849 CAGAAATCCATTCATCATCAAGTCCATGCGCGCGCCGACAGTACCCTCCAGCGGTCG 790
|
|
|
QY 1018 CTGCGGAGACACGTTGGCTGACCGGACAGTTGGCCGATCAGACAGTGGACAGACCGG 1077
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|
Db 789 CTGCGGAGACACGTTGGCTGACCGGACAGTTGGCCGATCAGACAGTGGACAGACCGG 730
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QY 1078 ACAATAGAAGAGAGACAGACCGCGCGGACCGCCGAGTAGAGTGCATGTCACGCT 1137
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|
|
Db 729 ACAATAGAAGAGAGAGACAGACCGCGCGGACCGCCGAGTAGAGTGCATGTCACGCT 670
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|
|
QY 1138 AGCTTACCTTTTTCAGAGCGCTGCTGTAAATACGTAAGCCCTTCCCAAGCGAGGCA 1197
|
|
|
Db 669 AGCTTACCTTTTTCAGAGCGCTGCTGTAAATACGTAAGCCCTTCCCAAGCGAGGCA 610
|
|
|
QY 1138 GGGGGGAGAGATGCTCAGCTAGCAGAGAGAGTGGCTAGCACTAGCA 1247
|
|
|
Db 609 GGGGGGAGAGATGCTCAGCTAGCAGAGAGAGTGGCTAGCACTAGCA 560
|
|
|

RESULT 6

CC678977 647 bp DNA linear GSS 19-JUN-2003
LOCUS OGJA129TV.ZM.0.7.1.5.KB.Zea.mays.genomic.clone.ZM5BMA0294B09,
DEFINITION genomic survey sequence.
ACCESSION CC678977
VERSION CC678977.1 GI:32083753
KEYWORDS GSS.

SOURCE

ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 647)
White, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Kohling, T.,
Citek, R.W., Numborg, A., Robbins, D., and Lakey, N.,
Consortium for Maize Genomics
Unpublished (2002)
Contact: Cathy Whitelaw

REFERENCE

AUTHORS Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Kohling, T.,
Citek, R.W., Numborg, A., Robbins, D., and Lakey, N.,
Consortium for Maize Genomics
Unpublished (2002)
Contact: Cathy Whitelaw

TITLE

JOURNAL

COMMENT

TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@cigr.org
Seq primer: TP
Clas: sheared ends.

FEATURES

source

1. 647
Location/Qualifiers
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZM5BMA0294B09"
/clone_lib="ZM 0.7-1.5 KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN

Query Match 20.2%; Score 251.4; DB 29; Length 647;
Best Local Similarity 99.2%; Pred. No. 7.6e-42;
Matches 263; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 993 CATGGCGCGCGGCGACGTAACCATCCAGCGGCTGCTCGGAGACAGTGTGGCTGAC 1042
|
|
|
Db 1 CATGGCGCGCGGCGACGTAACCATCCAGCGGCTGCTCGGAGAC-CTTGTGGCTGAC 59
|
|
|
QY 1043 CGGACAGTTGGCCGATTCAGACAGTGGACAGACCGGACATAGAGAGAGAGAGAGAG 1102
|
|
|
Db 60 CGGACAGTTGGCCGATTCAGACAGTGGACAGACCGGACATAGAGAGAGAGAGAGAG 119
|
|
|
QY 1103 GCGGCGGACCGGCGAGTAGTGTGATGCTACGCTGTAAGCTTTTTCAGAGCGTCG 1162
|
|
|
Db 120 GCGGCGGACCGGCGAGTAGTGTGATGCTACGCTGTAAGCTTTTTCAGAGCGTCG 179
|
|
|
QY 1163 TCTGTAATACGTAAGCCCTTTCACAAGGAGGCAAGGGGGAGAGATGTCAGCTAG 1222
|
|
|
Db 180 TCTGTAATACGTAAGCCCTTTCACAAGGAGGCAAGGGGGAGAGATGTCAGCTAG 239
|
|
|
QY 1223 CAGAGAGAGTGGTAGCAACTAGCA 1247
|
|
|

|||||
Db 240 CAGAGAGAGTGGCTAGCAACTAGCA 264

RESULT 7
CG155338
LOCUS PUIH26TB_ZM_0.6_1.0_KB_Zea_mays genomic clone ZMMBTa0589F04,
DEFINITION genomic survey sequence.
ACCESSION CG155338
VERSION CG155338.1 GI:34046139
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 860)
REFERENCE Whitehaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,
AUTHORS Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bennetzen,J.
TITLE Maize Genomics Consortium
JOURNAL Unpublished (2003)
COMMENT Other GSSs: PUIH26TD
Contact: Cathy Whitehaw
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitehaw@tigr.org
Seq primer: TR
Class: sheared ends.
FEATURES
source Location/Qualifiers
1..860
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone_lib="ZMMBTa0589F04"
/clone_lib="ZM_0.6_1.0_KB"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"

Query Match 16.2%; Score 201.8; DB 29; Length 860;
Best Local Similarity 84.2%; Pred. No. 1.3e-31;
Matches 240; Conservative 0; Mismatches 42; Indels 3; Gaps 1;

QY 525 AACCGATGTGGAGACAATTTTCTAGTGTAAGTCACTGATGATTAAT 584
|||
Db 107 AACCGATGTGGAGACAATTTTCTAGTGTAAGTCACTGATGATTAAT 166
|||
QY 585 AATATTTTCACATGCGGTTTCTTAAGCAAAACCGCAGTGTATGATTTTACACTAGCG 644
|||
Db 167 AATATTTTCACATGCGGTTTCTTAAGTAACTGCGAGTGTATGATTTTACACTAGCG 226
|||
QY 645 GGGTGTAAAGAAACCGCCGCTGCTAAAGATATTACACTAGCGGTTGTGAACAATG 704
|||
Db 227 GGGAGCTAAAGAAACCGTCAAGTGTAAATGATATTACACTGCGGTTGTGAACAACA 286
|||
QY 705 CCTGTGAAAAAAGCCGATTTCTACTAGCCCTTACGCTTGACATGCGACATAAAAACGTC 764
|||
Db 287 CCTGTGAAAAAAGCAATTTTCTACTAGCCCTTACGAT--TGCGGACACTGAAAAACGCC 343
|||
QY 765 AGTGAATAATAGCTCTAGATCGTCACTATAGAGCTTCTATGTAAT 809
|||
Db 344 AGTGCAATAGCTCTTAGAGACCGCCACTATAGAGCTTCCGTGTAAT 388
|||

RESULT 8
CG037363/c
LOCUS PUFN159TD_ZM_0.6_1.0_KB_Zea_mays genomic clone ZMMBTa0690122,
DEFINITION

genomic survey sequence.
CG037363
VERSION CG037363.1 GI:33909519
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 861)
REFERENCE Whitehaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,
AUTHORS Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bennetzen,J.
TITLE Maize Genomics Consortium
JOURNAL Unpublished (2003)
COMMENT Other GSSs: PUFN159TB
Contact: Cathy Whitehaw
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitehaw@tigr.org
Seq primer: TR
Class: sheared ends.
FEATURES
source Location/Qualifiers
1..861
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone_lib="ZMMBTa0690122"
/clone_lib="ZM_0.6_1.0_KB"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"

Query Match 15.5%; Score 193; DB 29; Length 861;
Best Local Similarity 84.6%; Pred. No. 8.9e-30;
Matches 241; Conservative 0; Mismatches 40; Indels 4; Gaps 2;

QY 525 AACCGATGTGGAGACAATTTTCTAGTGTAAGTCACTGATGATTAAT 584
|||
Db 606 AACCGATGTGGAGACAATTTTCTAGTGTAAGTCACTGATGATTAAT 548
|||
QY 585 AATATTTTCACATGCGGTTTCTTAAGCAAAACCGCAGTGTATGATTTTACACTAGCG 644
|||
Db 547 AATATTTTCACATGCGGTTTCTTAAGCAAAACCGCAGTGTATGATTTTACACTAGCG 488
|||
QY 645 GGGTGTAAAGAAACCGCCGCTGCTAAAGATATTACACTAGCGGTTGTGAACAATG 704
|||
Db 487 GGGTGTAAAGAAACCGCAGTGTAAATGATTTGACGTTGACAAACAACCG 428
|||
QY 705 CCTGTGAAAAAAGCCGATTTCTACTAGCCCTTACGCTTGACATGCGACATAAAAACGTC 764
|||
Db 427 CCTGTGAAAAAAGCCGATTTCTACTAGCCCTTACGACACTGAC---GGCACTGAAAAATGCG 371
|||
QY 765 AGTGAATAATAGCTCTAGATCGTCACTATAGAGCTTCTATGTAAT 809
|||
Db 370 AGTATTAATAGCTCTTAGAGACCGACACTATAGAGCTTCTGTGTAAT 326
|||

RESULT 9
CG098858/c
LOCUS PUFQ026TD_ZM_0.6_1.0_KB_Zea_mays genomic clone ZMMBTa0769F03,
DEFINITION genomic survey sequence.
ACCESSION CG098858
VERSION CG098858.1 GI:33981152
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 872)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,
Rennick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
Maize Genomics Consortium
Unpublished (2003)
Other GSSs: PUFQ26TB
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.

FEATURES
source
Location/Qualifiers

1..872
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZM87A0769F03"
/clone_1lb="ZM_0.6_1.0_KB"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
Cot selected genomic DNA library"

ORIGIN

Query Match 15.3%; Score 191.4; DB 29; Length 872;
Best Local Similarity 84.2%; Pred. No. 1.9e-29;
Matches 240; Conservative 0; Mismatches 41; Indels 4; Gaps 2;

QY 525 AACCGATGAGAGACAATTTTCATAGTGTACTGTTTAAGTCAACCGTCAGTATAT 584
DB 653 AACCGATGAGAGACAATTTTCATAGTGTACTGTTTAAGTCAACCGTCAGTATAT 595
QY 585 AATATTTTCCACATGCGGCTTTCTTAAGCAAAACCGCAGTCTAATGATTTTACATAGCG 644
DB 594 AATATTTTCCACATGCGGCTTTCTTAAGCAAAACCGCAGTCTAATGATTTTACATAGCG 535
QY 645 GGCTGCTAAAGAAAACCGCCGCTGCTAAAGATTTTACACTAGCGTTGGTGAACAACG 704
DB 534 GGCTGCTAAAGAAAACCGCCAGTCTAATGATTTTGAATGACGCTTGAACAACAACG 475
QY 705 CCTGTGAAAAAAGCCGATTCCTACTAGCCCTAGCTTGCACCTGGCGACATAAAAACGTC 764
DB 474 CCTGTGAAAAAAGCCGATTCCTACTAGCCCTAGCTTGCACCTGGCGACATAAAAACGTC 418
QY 765 AGTGAATAATAGCTCTAGATCGTCACTATATAGAGCTTCTATGTAAT 809
DB 417 AGTGAATAATAGCTCTAGATCGTCACTATATAGAGCTTCTATGTAAT 373

RESULT 10
LOCUS CG455835 884 bp DNA linear GSS 17-SBP-2003
DEFINITION PUFQ077DB ZM 0.6_1.0_KB Zea mays genomic clone ZM87A0602B13,
genomic survey sequence.
ACCESSION CG455835
VERSION CG455835.1 GI:34840835
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 884)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,
Rennick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
Maize Genomics Consortium
Unpublished (2003)
Other_GSSs: PUFQ077DB

Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.
Location/Qualifiers

FEATURES
source
1..884
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZM87A0602B13"
/clone_1lb="ZM_0.6_1.0_KB"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
Cot selected genomic DNA library"

ORIGIN

Query Match 15.3%; Score 191.4; DB 29; Length 884;
Best Local Similarity 84.2%; Pred. No. 1.9e-29;
Matches 240; Conservative 0; Mismatches 41; Indels 4; Gaps 2;

QY 525 AACCGATGAGAGACAATTTTCATAGTGTACTGTTTAAGTCAACCGTCAGTATAT 584
DB 646 AACCGATGAGAGAGACAATTTTCATAGTGTACTGTTTAAGTCAACCGTCAGTATAT 588
QY 585 AATATTTTCCACATGCGGCTTTCTTAAGCAAAACCGCAGTCTAATGATTTTACATAGCG 644
DB 587 AATATTTTCCACATGCGGCTTTCTTAAGCAAAACCGCAGTCTAATGATTTTACATAGCG 528
QY 645 GGCTGCTAAAGAAAACCGCCGCTGCTAAAGATTTTACACTAGCGTTGGTGAACAACG 704
DB 527 GGCTGCTAAAGAAAACCGCCAGTCTAATGATTTTGAATGACGCTTGAACAACAACG 468
QY 705 CCTGTGAAAAAAGCCGATTCCTACTAGCCCTAGCTTGCACCTGGCGACATAAAAACGTC 764
DB 467 CCTGTGAAAAAAGCCGATTCCTACTAGCCCTAGCTTGCACCTGGCGACATAAAAACGTC 411
QY 765 AGTGAATAATAGCTCTAGATCGTCACTATATAGAGCTTCTATGTAAT 809
DB 410 AGTGAATAATAGCTCTAGATCGTCACTATATAGAGCTTCTATGTAAT 366

RESULT 11
LOCUS BZ795791 889 bp DNA linear GSS 17-MAR-2003
DEFINITION PUFQ22TB ZM 0.6_1.0_KB Zea mays genomic clone ZM87A314C19,
genomic survey sequence.
ACCESSION BZ795791
VERSION BZ795791.1 GI:28996519
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 889)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,
Rennick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
Maize Genomics Consortium
Unpublished (2003)
Other_GSSs: PUFQ22TD
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.

FEATURES
source
Location/Qualifiers
1.889
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone_lib="ZM0614C19"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"

Query Match 15.3%; Score 191.4; DB 28; Length 889;
Best Local Similarity 84.2%; Pred. No. 1.9e-29;
Matches 240; Conservative 0; Mismatches 41; Indels 4; Gaps 2;

QY 525 AACCGTATGTGAGACACATTTTCATAGGTGTTTAACTACCGCTAGTATAT 584
DB 420 AACCGTATGTAGAGACACATTTTCATAGGCG-GCTGCTTAAGACACCGCGATATAT 478
QY 585 AATATTTTCACTGCGGTTTCTTAAGCAACCGCCAGTGTATATTTTACACTAGCG 644
DB 479 AATATTTTCCACATGCGGCTTCTTAAGCAACCGCCAGTGTATATTTTACATTAGCG 538
QY 645 GGCTGCTAAAGAAACCGCCGCTTAAGATATTTACACTAGCGGTGTGACAACTG 704
DB 539 GGCTGCTAAAGTAAACCGCCAGTGTATATTTTGCATGACGGTGTGACAAACCG 598
QY 705 CCTGTGAAAAAGCCGATTCCTTACTAGCCCTAGCTTGACCTGGACATTAATAACGTC 764
DB 599 CCTGTGAAAAAGCCGATTCCTTACTAGCCCTAGCTGAC---GGCACTGAAAAATGCC 655
QY 765 AGTGAATAATGCTCTAGATGCTGCTACTATAGAGCTTCTATGACT 809
DB 656 AGTGAATAATGCTCTAGAGCCGACACTATATAGAGCTTCTGTACT 700

RESULT 12
#BZ795799/c 891 bp DNA linear GSS 17-MAR-2003
LOCUS PUFGM22TD ZM 0.6 1.0 KB Zea mays genomic clone ZMBR1314C19,
DEFINITION genomic survey sequence.
ACCESSION BZ795799
VERSION BZ795799.1 GI:28996535
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 891)
White, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
Maize Genomics Consortium
Unpublished (2003)
Other_GSSs: PUFGM22TB
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.
Location/Qualifiers
1.891
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone_lib="ZMBR1314C19"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"

FEATURES
source

ORIGIN
/note="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"

Query Match 15.3%; Score 191.4; DB 28; Length 891;
Best Local Similarity 84.2%; Pred. No. 1.9e-29;
Matches 240; Conservative 0; Mismatches 41; Indels 4; Gaps 2;

QY 525 AACCGTATGTGAGACACATTTTCATAGGTGTTTAACTACCGCTAGTATAT 584
DB 670 AACCGTATGTAGAGACACATTTTCATAGGCG-GCTGCTTAAGACACCGCGATATAT 612
QY 585 AATATTTTCACTGCGGTTTCTTAAGCAACCGCCAGTGTATATTTTACACTAGCG 644
DB 611 AATATTTTCCACATGCGGCTTCTTAAGCAACCGCCAGTGTATATTTTACATTAGCG 552
QY 645 GGCTGCTAAAGAAACCGCCGCTTAAGATATTTTACACTAGCGGTGTGACAACTG 704
DB 551 GGCTGCTAAAGTAAACCGCCAGTGTATATTTTGCATGACGGTGTGACAAACCG 492
QY 705 CCTGTGAAAAAGCCGATTCCTTACTAGCCCTAGCTTGACCTGGACATTAATAACGTC 764
DB 491 CCTGTGAAAAAGCCGATTCCTTACTAGCGCCCTAGCACTGAC---GGCACTGAAAAATGCC 435
QY 765 AGTGAATAATGCTCTAGATGCTGCTACTATAGAGCTTCTATGACT 809
DB 434 AGTGAATAATGCTCTAGAGCCGACACTATATAGAGCTTCTGTACT 390

RESULT 13
#BZ786431 856 bp DNA linear GSS 17-MAR-2003
LOCUS PUGB229TB ZM 0.6 1.0 KB Zea mays genomic clone ZMBR1327F10,
DEFINITION genomic survey sequence.
ACCESSION BZ786431
VERSION BZ786431.1 GI:28980028
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 856)
White, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
Maize Genomics Consortium
Unpublished (2003)
Other_GSSs: PUGB229TB
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
1.856
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone_lib="ZMBR1327F10"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"

ORIGIN
Query Match 15.3%; Score 190.6; DB 28; Length 856;
Best Local Similarity 81.8%; Pred. No. 2.8e-29;
Matches 233; Conservative 0; Mismatches 49; Indels 3; Gaps 1;

OY	525	AACCGTAGTGGAGCAACATTTTCATGAGTGTAAGTACCCTCAGTAGTAAT	584
Db	144	AACCGCATGTGGAACATCATTTTTACAGCGCGTGTCTTAAGCACACCACTGATTAAIT	203
OY	585	AATAATTTTCACATGCGGTTTCTTAAGCAAACCCGCAAGTCTAATGATATTTAACACTAGCG	644
Db	204	ATTATATTTTATATGTGGGTTTCTTAAACAAACCGCAGTCTAATGATATTTTACACTGCTG	263
OY	645	GCGTCTTAAAGAAAACCGCCCGTGCTAAAGATATTATACATGACGGTGTGTAAACAACG	704
Db	264	GTTCTCTTAAAGAAAACCGTCAAGTGAATATGTATTATTTACCTGGCTGTGTGGCAAACAACG	323
OY	705	CCTGTGAAAAAAGCCGATTTCTACTAGCCCCCTAGCTTGCATCGCGACATTAAAAAACGTC	764
Db	324	CCTGTGAAAAAAGCCGATTTCTACTAGCCCCCTA---ATACGTGTGGCACTGAAAAACGAC	380
OY	765	AGTGAATAATAGCTTAGAGTGTGACTATATATATATATATATATATATATATATATATAT	809
Db	381	AGTGAATAATAGCTTAGAGTGTGACTATATATATATATATATATATATATATATATATAT	425

[illegible]

9112 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: white1a@white1a.org
Seq Primer: TP
Class: sheared ends.
Location/Qualifiers
1. .844

FEATURES	source	Location/Qualifiers
	1..844	
	/organism="Zea mays"	
	/mol_type="genomic DNA"	
	/strain="B73"	
	/db_xref="Btakon:4577"	
	/clone="ZMMB7A214B14"	
	/clone_1b="ZM_0.6-1.0_KB"	
	/note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high Cot selected genomic DNA library"	
ORIGIN		

Query Match	15.0%	Score 187.4	DB 28	Length 844
Best Local Similarity	81.1%	Pred. No. 1.3e+28		
Matches 231	0	Mismatches 51	Indels 3	Gaps 1

332 AACCGCATGCGAGCAACATTTTCATAGCGTACTGTTTAAGTACCGTCAGTGCTAAT 584

585 AATAATTTTCACATGCGGTTTCTTAAGCAAAACGCCAGTGCTAATGATATTTACACTAGCG 644

db 392 AATATTTTTCACATCTGATTTTCTTAACTAAACCGCCAGTGCATAATGATTTTACACAGCG 451
oy 585 AATATTTTTCACATCGTTTCTTAAGCAACCGCCAGTGCATAATGATTTTACACAGCG 644

615 GGCTCTAAAGAAACCGCCCGTGCTAAAGATATTTACACTTAGCGGTGGTGACAACTG 704

Accession	Sequence	Position
D8	GGCTGCTAAAGAAAACACCACTGATTAATGTTATTATTAACCTGGCGGTGGGAAACAAACCG	51111
OY	CCTGTGAAAAAGCCGATTCCTACTAGCCCTAGCTTGCACTGGCAATTAATAACGTC	764
D8	CCGTGTAAGAAAGGTCATTTCTACGACCCCAATGC--ACTGGGGGCACTGGAAAAAGCC	568
OY	AGTGAATAATAGCTCTAGATGCTGCTACTATAGAGCTTCATATTA	809
D8	AGTGCATAATAGCTTTAGAACCCCACTATAGAGCTTCGTGTACT	613

RESULT	15
CG132370	
LOCUS	
DEFINITION	905 bp DNA linear GSS 21-AUG-2003 PUUGH42TB ZM 0.6 1.0 KB Zea mays genomic clone ZMMBRT0661H12, genomic survey sequence.
ACCESSION	CG132370
VERSION	CG132370.1 GI:34019817
KEYWORDS	GSS.
SOURCE	Zea mays

REFERENCE
AUTHORS

WhiteIaw, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,
1 (bases 1 to 905)
clade; Panicoideae; Andropogoneae; Zea.

TITLE	Maize Genomics Consortium
JOURNAL	unpublished (2003)
COMMENT	Other_GSSs: PUGGH42TD
	Contact: Cathy Whitelaw
	TIGR

9112 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: white.law@tigr.org
Seq primer: TR
Class: sheared ends.

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Matches 231; Conservative	0;	Mismatches 51;	Indels 3;	Gaps 1

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